



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 165876

TO: Suzanne M Mayer
Location: REM/3E84/3C70
Art Unit: 1653

Sept 17, 2005

Case Serial Number: 10/795795

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

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From: Chan, Christina
Sent: Thursday, September 15, 2005 3:25 PM
To: Mayer, Suzanne Marie; STIC-Biotech/ChemLib
Subject: RE: Rush 10/795795

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Mayer, Suzanne Marie
Sent: Thursday, September 15, 2005 2:22 PM
To: Chan, Christina
Subject: RE: Rush 10/795795

Chris,

Could I get these two small peptides rushed through please on this special case, I had sent it previously, but they have come in with new proposed min. and max. length requirements.

Thank you!!!!!!!

Dear search staff:

Factor Va aa 322-331
352-356
Please search SEQ ID NO: 6 (10 amino acids) and SEQ ID NO:12 (5 amino acids) against amino-acid-databases-in-both commercial and interference databases. *** Please limit the search to a minimum length of 3 and a maximum length of 10.

Please call with any questions.

Suzy

Suzanne M. Mayer, Ph.D.
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United States Patent and Trademark Office
400 Dulany St. - Remsen
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AU 1653: 3 E 84
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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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4th 102E
(322-331)

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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:42:23 ; Search time 155.333 Seconds
(without alignments)
24.899 Million cell updates/sec

Title: US-10-795-795-6
Perfect score: 55
Sequence: 1 WEYFIAAEV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 464945

Minimum DB seq length: 3
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1980s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	55	100.0	10	6 ABU62020	Abu62020 Human blo
2	55	100.0	10	8 ADS64542	Ads64542 Human blo
3	33	60.0	10	6 ABU62019	Abu62019 Human blo
4	33	60.0	10	8 ADS64541	Ads64541 Human blo
5	29	52.7	9	4 AAY72469	Aay72469 Human DNA
6	29	52.7	9	4 AAG63594	Aag63594 Peptide d
7	27	49.1	9	2 AAW03705	Aaw03705 Lys (4), D
8	27	49.1	10	5 ABG5739	Abg5739 Plant ICK
9	26	47.3	6	2 AAW78369	Aaw78369 Isoelectr
10	26	47.3	6	5 ABR82656	Abg79015 Immune-mo
11	26	47.3	6	7 ABR82656	Abg79015 Immune-mo
12	26	47.3	9	1 AAP20184	Aap20184 Sequence
13	26	47.3	9	1 AAP30521	Aap30521 Sequence
14	26	47.3	9	2 AAY46157	Aay46157 Immunogen
15	26	47.3	9	2 AAY45504	Aay45504 Immunogen
16	26	47.3	9	2 AAY46158	Aay46158 Immunogen
17	26	47.3	9	2 AAY46170	Aay46170 Immunogen
18	26	47.3	9	2 AAY00813	Aay00813 HLA-A24 a
19	26	47.3	9	4 AAG84792	Aag84792 MAGE3 HLA
20	26	47.3	9	7 ADE68466	Ade68466 Human 161
21	26	47.3	9	7 ADE68415	Ade68415 Human 161
22	26	47.3	9	7 ADE68608	Ade68608 Human 161
23	26	47.3	9	7 ADE68799	Ade68799 Human 161
24	26	47.3	9	7 ADE68739	Ade68739 Human 161
25	26	47.3	9	7 ADE68096	Ade68096 Human 161

26	47.3	9	7	ADS68258	Ade68258 Human 161
27	47.3	9	7	ADS66983	Ade66983 Human 161
28	47.3	9	7	ADS68740	Ade68740 Human 161
29	47.3	9	7	ADS68884	Ade68884 Human 161
30	47.3	9	7	ADS67039	Ade67039 Human 161
31	47.3	9	7	ADS69145	Ade69145 Human 161
32	47.3	9	7	ADS66327	Ade66327 Human 161
33	47.3	9	7	ADS66789	Ade66789 Human 161
34	47.3	9	7	ADS68257	Ade68257 Human 161
35	47.3	9	7	ADS66236	Ade66236 Human 161
36	47.3	9	7	ADS66483	Ade66483 Human 161
37	47.3	9	7	ADS67782	Ade67782 Human 161
38	47.3	9	7	ADS68414	Ade68414 Human 161
39	47.3	9	7	ADG38678	Adg38678 Human mel
40	47.3	9	8	ADG89583	Adg89583 Class I H
41	47.3	9	8	ADP80081	Adp80081 Human HLA
42	47.3	10	1	AAP10167	Aap10167 Sequence
43	47.3	10	1	AAP30391	Aap30391 Gonadotro
44	47.3	10	1	AAP50839	Aap50839 Sequence
45	47.3	10	1	AAP50509	Aap50509 Sequence

ALIGNMENTS

RESULT 1
ABU62020
ID ABU62020 standard; peptide; 10 AA.

XX ABU62020;
XX AC
XX XX
DT 26-AUG-2003 (first entry)
XX XX
DE Human blood coagulation factor Va peptide, AP4.

XX Human; blood coagulation factor Va; blood clotting factor Va;
KW prothrombinase inhibition; prothrombinase-inhibiting peptide;
KW blood clotting disorder; thrombotic disorder; blood clot formation;
KW blood vessel obstruction; coronary artery disease; unstable angina;
KW valvular heart disease; stable angina; myocardial infarction;
KW atrial fibrillation; stroke; blood anticoagulation; anticoagulant.

XX Homo sapiens.

XX US2003040600-A1.

XX 27-FEB-2003.

XX 23-JUL-2001; 2001US-00911129.

XX 23-JUL-2001; 2001US-00911129.

XX (KALA/) KALAFATIS M.

XX (MANN/) MANN K.

XX Kalafatis M, Mann K;

XX WPI; 2003-492177/46.

XX Novel anticoagulant peptide derived from the amino acid region 307-356 of human blood clotting factor Va, useful for preventing thrombotic disorders resulting from formation of blood clots that obstruct blood vessels.

XX Claim 10; Fig 2; 20pp; English.

XX The present invention relates to peptides derived from human blood coagulation (clotting) factor Va which exhibit inhibition of prothrombinase. A pharmaceutical composition comprising one or more of the prothrombinase-inhibiting peptides may be used for treating human subjects with blood clotting disorders. The peptides are useful for preventing thrombotic disorders resulting from the formation of blood clots that obstruct blood vessels, e.g. due to a condition chosen from

CC coronary artery disease, valvular heart disease, stable and unstable
 CC angina, myocardial infarction, atrial fibrillation and stroke. The
 CC peptides of the invention exhibit an IC50 of between 50 nanoM-500 microM
 CC for inhibition of prothrombinase. The peptides exhibit excellent blood
 CC anticoagulation properties with little or no adverse side effects. The
 CC present sequence represents a peptide that inhibits prothrombinase
 CC activity
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 55; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0029; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;
 QY 1 WEYFIAAEV 10
 Db |||||
 1 WEYFIAAEV 10
 RESULT 2
 ADS64542
 ID ADS64542 standard; peptide; 10 AA.
 XX
 AC ADS64542;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human blood coagulation factor Va peptide, AP4.
 XX
 KW Prothrombinase inhibitor; human; blood coagulation factor Va;
 KW blood clotting disorder; thrombotic disorder; thrombolytic.
 XX
 OS Homo sapiens.
 XX
 PN US2004186271-A1.
 XX
 PD 23-SEP-2004.
 XX
 PF 08-MAR-2004; 2004US-00795795.
 XX
 PR 23-JUL-2001; 2001US-00911129.
 XX
 PA (KALA/) KALAFATIS M.
 PA (MANN/) MANN K G.
 XX
 PI Kalafatis M, Mann KG;
 DR WPI; 2004-689241/67.
 XX
 XX New prothrombinase-inhibiting peptide derived from a specific amino acid
 PT sequence of human blood coagulation factor Va, useful for treating human
 PT subjects with blood clotting disorders.
 XX
 PS Claim 10; SEQ ID NO 6; 20pp; English.
 XX
 CC The present invention relates to a prothrombinase-inhibiting peptide
 CC derived from a specific amino acid sequence of human blood coagulation
 CC factor Va. The invention is useful for treating human subjects with blood
 CC clotting disorders. The invention is also useful for preventing
 CC thrombotic disorders resulting from formation of blood clots that
 CC obstructs blood vessels. The present sequence is the human blood
 CC coagulation factor Va peptide.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 55; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0029; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;
 QY 1 WEYFIAAEV 10
 Db |||||
 1 WEYFIAAEV 10

RESULT 3
 ABUG2019
 ID ABUG2019 standard; peptide; 10 AA.
 XX
 AC ABUG2019;
 XX
 DT 26-AUG-2003 (first entry)
 XX
 DE Human blood coagulation factor Va peptide, AP3.
 XX
 KW Human; blood coagulation factor Va; blood clotting factor Va;
 KW prothrombinase inhibition; prothrombinase-inhibiting peptide;
 KW blood clotting disorder; thrombotic disorder; blood clot formation;
 KW blood vessel obstruction; coronary artery disease; unstable angina;
 KW valvular heart disease; stable angina; myocardial infarction;
 KW atrial fibrillation; stroke; blood anticoagulation; anticoagulant.
 XX
 OS Homo sapiens.
 XX
 PN US2003040600-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 23-JUL-2001; 2001US-00911129.
 XX
 PR 23-JUL-2001; 2001US-00911129.
 XX
 PA (KALA/) KALAFATIS M.
 PA (MANN/) MANN K.
 XX
 PI Kalafatis M, Mann K;
 DR WPI; 2003-492177/46.
 XX
 PT Novel anticoagulant peptide derived from the amino acid region 307-356 of
 PT human blood clotting factor Va, useful for preventing thrombotic
 PT disorders resulting from formation of blood clots that obstruct blood
 PT vessels.
 XX
 PS Claim 10; Fig 2; 20pp; English.
 XX
 CC The present invention relates to peptides derived from human blood
 CC coagulation (clotting) factor Va which exhibit inhibition of
 CC prothrombinase. A pharmaceutical composition comprising one or more of
 CC the prothrombinase-inhibiting peptides may be used for treating human
 CC subjects with blood clotting disorders. The peptides are useful for
 CC preventing thrombotic disorders resulting from the formation of blood
 CC clots that obstruct blood vessels, e.g. due to a condition chosen from
 CC coronary artery disease, valvular heart disease, stable and unstable
 CC angina, myocardial infarction, atrial fibrillation and stroke. The
 CC peptides of the invention exhibit an IC50 of between 50 nanoM-500 microM
 CC for inhibition of prothrombinase. The peptides exhibit excellent blood
 CC anticoagulation properties with little or no adverse side effects. The
 CC present sequence represents a peptide that inhibits prothrombinase
 CC activity
 XX
 SQ Sequence 10 AA;
 Query Match 60.0%; Score 33; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 29; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;
 QY 1 WEYFI 5
 Db |||||
 6 WEYFI 10
 RESULT 4
 ADS64541
 ID ADS64541 standard; peptide; 10 AA.
 XX
 AC ADS64541;

XX 16-DEC-2004 (first entry)
XX Human blood coagulation factor Va peptide, AP3.
XX Prothrombinase inhibitor; human; blood coagulation factor Va;
KW blood clotting disorder; thrombotic disorder; thrombolytic.
XX Homo sapiens.
XX US2004186271-A1.
XX 23-SEP-2004.
XX 08-MAR-2004; 2004US-00795795.
XX 23-JUL-2001; 2001US-00911129.
XX (KALA/) KALAFATIS M.
XX (MANN/) MANN K G.
XX Kalafatis M, Mann KG;
XX WPI; 2004-689241/67.
XX New prothrombinase-inhibiting peptide derived from a specific amino acid
PT sequence of human blood coagulation factor Va, useful for treating human
PT subjects with blood clotting disorders.
XX Claim 10; SEQ ID NO 5; 20pp; English.
XX The present invention relates to a prothrombinase-inhibiting peptide
CC derived from a specific amino acid sequence of human blood coagulation
CC factor Va. The invention is useful for treating human subjects with blood
CC clotting disorders. The invention is also useful for preventing
CC thrombotic disorders resulting from formation of blood clots that
CC obstruct blood vessels. The present sequence is the human blood
CC coagulation factor Va peptide.
XX Sequence 10 AA;
XX Query Match 60.0%; Score 33; DB 8; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 29;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WEYFI 5
DB 6 WEYFI 10
RESULT 5
AAV72469
ID AAV72469 standard; peptide; 9 AA;
XX AAV72469;
AC AAV72469;
XX 24-APR-2001 (first entry)
XX Human DNA fragmentation factor 40 (DFF40) derived peptide #1.
XX Human; DNA fragmentation factor; DFF; apoptosis; molecular chaperone;
KW gene therapy; hyperproliferative disorder; therapy; tumour; restenosis;
KW psoriasis; angiogenesis; cancer; cytostatic; neoplasia.
XX Homo sapiens.
XX US6165737-A.
XX 26-DEC-2000.
XX 16-APR-1998; 98US-00061702.
XX 16-APR-1998; 98US-00061702.
XX 16-APR-1998; 98US-00061702.

XX (TEXA) UNIV TEXAS SYSTEM.
XX Wang X, Liu X;
XX WPI; 2001-090481/10.
XX Identifying modulator of human DNA fragmentation factor 40, for treating
PT cancer, involves contacting cell or cell-free composition comprising
PT DFF40 with candidate substance and comparing apoptosis with control.
XX Example 1; Col 63; 52pp; English.
XX The present sequence is a human DNA fragmentation factor 40 (DFF40)
CC derived peptide. DFF is a heterodimeric protein comprising 40KDa and
CC 45KDa subunits. DFF40 is capable of inducing apoptosis. DFF45 acts as a
CC molecular chaperone to facilitate the appropriate folding of DFF40 and
CC acts as an inhibitor for DFF40. DFF40 and DFF45 are used in gene therapy.
CC The modulators of human DFF40 activity are useful for inducing apoptosis
CC and for treating hyperproliferative disorders such as restenosis,
CC psoriasis, metastatic tumours, angiogenesis and benign and malignant
CC neoplasias. They are also used for treating cancers of the brain
CC (glioblastoma, astrocytoma, oligodendroglioma and ependymoma), lung,
CC liver, spleen, kidney, lymph node, pancreas, small intestine, blood
CC cells, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone marrow, blood, other tissue and
CC multi-drug resistant cancer
XX Sequence 9 AA;
XX Query Match 52.7%; Score 29; DB 4; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WEYF 4
DB 4 WEYF 7
RESULT 6
AAG63594
ID AAG63594 standard; peptide; 9 AA.
XX AAG63594;
AC AAG63594;
XX 15-OCT-2001 (first entry)
XX Peptide derived from human DNA fragmentation factor 40 (DFF40).
DE Human; DNA fragmentation factor; DFF40; DFF45; apoptosis; DNase;
KW molecular chaperone; cancer cell.
XX Homo sapiens.
XX US2001011078-A1.
XX 02-AUG-2001.
XX 22-DEC-2000; 2000US-00748451.
XX 16-APR-1998; 98US-00061702.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Wang X, Liu X;
XX WPI; 2001-496169/54.
XX New DNA fragmentation factor polypeptides and polynucleotides, useful for
PT inhibiting the growth of cancer cells, as well as for inducing apoptosis
PT of cells.
XX Example 1; Page 19; 56pp; English.

XX The present sequence represents a peptide, derived from human DNA
 CC fragmentation factor subunit of 40 kDa, designated DFF40. The peptide was
 CC used to design a PCR primer (AAH74644). The specification also describes
 CC DFF45. DFF40 is capable of inducing apoptosis, and may contain a nuclear
 CC localisation fragment. DFF45 acts as a molecular chaperone to direct the
 CC folding of DFF40. Although all DNase activity is associated with DFF40,
 CC DFF activity only occurs once DFF40 is complexed with DFF45. The DFF
 CC polypeptides and polynucleotides are useful for inhibiting the growth of
 CC cancer cells, and for inducing apoptosis of cells
 XX
 SQ Sequence 9 AA;
 Query Match 52.7%; Score 29; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WEYF 4
 Db 4 WEYF 7
 RESULT 7
 AA03705
 ID AAW03705 standard; peptide; 9 AA.
 AC AAW03705;
 XX
 DT 25-FEB-1997 (first entry)
 DE Lys(4), D-Phe(6)-hGRH(1-9)-ethylamide.
 XX
 KW gonadotropin releasing hormone; GnRH; analogue; conjugate;
 KW poly(N-vinylpyrrolidone-co-maleic anhydride) polymer; breast cancer.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "pyro-Glu"
 FT Misc-difference 6 /note= "D-form residue"
 FT Modified-site 9 /note= "Pro-NH2"
 FT
 XX WO9604927-A1.
 XX
 PD 22-FEB-1996.
 XX
 PF 09-AUG-1995; 95WO-US010054.
 XX
 PR 10-AUG-1994; 94HU-00002328.
 PR 10-AUG-1994; 94HU-00002329.
 XX
 PA (LOVA/) LOVAS S.
 PA (MURP/) MURPHY R F.
 PA (TOTH/) TOTH G.
 PA (KALN/) KALNAY A.
 PA (GAAL/) GAAL D.
 PA (PALY/) PALYI I.
 PA (TURI/) TURI G.
 PA (VINC/) VINCZE B.
 PA (MEZO/) MEZO I.
 PA (TANA/) TANAI H.
 PA (VADA/) VADASZ Z.
 PA (TEPL/) TEPLAN I.
 PA (SEPR/) SEPRODI J.
 XX
 PI Lovas S, Murphy RF, Toth G, Kalnay A, Gaal D, Palyi I, Turi G;
 PI Vincze B, Mezo I, Tanai H, Vadasz Z, Teplan I, Seprodi J;
 XX
 DR WPI; 1996-139455/14.

PT New conjugates of active peptide(s) - are useful for inhibiting growth of
 PT cancers esp. breast cancer.
 XX
 PS Claim 15; Page 68; 70pp; English.
 XX
 CC Two new types of GnRH peptide molecules are provided. The first type
 CC consists of a poly(N-vinylpyrrolidone-co-maleic anhydride) polymer having
 CC conjugated to it a number of molecules of native GnRH or a GnRH analogue.
 CC Conjugation is by condensation between a carbonyl group attached to the
 CC polymer backbone and a side chain epsilon-amino group of a lys residue of
 CC the GnRH or its analogue. Optionally this condensation may be via the
 CC intermediary of a peptide spacer group (preferably -Gly-Phe-Leu-Gly-, -
 CC Phe-Leu-Gly-, Gly-Leu-Gly- or -Ala-). The second type consists of
 CC specific GnRH analogues which are themselves new and which can optionally
 CC be used as components of the above conjugate. Both types of molecule are
 CC useful as inhibitors of tumours, particularly breast cancer. The present
 CC sequence represents a specifically claimed example of the new GnRH
 CC analogues
 XX
 SQ Sequence 9 AA;
 Query Match 49.1%; Score 27; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WEYFI 5
 Db 3 WKYFL 7
 RESULT 8
 ABG65739
 ID ABG65739 standard; peptide; 10 AA.
 XX
 AC ABG65739;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Plant ICK protein conserved motif 1 #47.
 XX
 KW Plant; inhibitor of cyclin dependent kinase; ICK.
 KW Oryza sativa.
 OS
 XX WO200228893-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 29-JUN-2001; 2001WO-IB001492.
 XX
 PR 14-JUL-2000; 2000US-0218471P.
 PR 13-OCT-2000; 2000US-0241219P.
 XX
 PA (CROP-) CROPDESIGN NV.
 XX
 PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
 PI Hatzfeld Y;
 XX
 DR WPI; 2002-471311/50.
 XX
 PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterized by an insufficient or excessive production
 PT of ICK inhibitors.
 XX
 PS Disclosure; Page 14; 141pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to

CC treat disorders characterised by insufficient or excessive production of
CC ICK protein, forms which have decreased or aberrant activity compared to
CC ICK wild type protein. The present sequence represents an inhibitor of
CC cyclin dependent kinase (ICK) protein of the invention
XX
SQ Sequence 10 AA;

Query Match 49.1%; Score 27; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 EYFAAEE 9
DB 3 EAFPAEE 10

RESULT 9
AAW78369
ID AAW78369 standard; peptide; 6 AA.

AC AAW78369;
XX
XX 11-MAY-1999 (first entry)
DT
XX
XX Isoelectric focusing marker peptide #33.

XX Marker peptide; capillary isoelectric focusing electrophoresis; IEF; pI;
KW tryptophan; detection; UV absorption.
XX
XX Synthetic.

XX JP11023531-A.
PN
XX 29-JAN-1999.
PD
XX 03-JUL-1997; 97JP-00178579.
PF
XX 03-JUL-1997; 97JP-00178579.
PR

XX (BUNS-) BUNSHI BIOHOTOINICS KENKYUSHO KK.
PA
XX WPI; 1999-170244/15.
DR

XX Markers for isoelectric point electrophoresis in UV absorption detection
PT - contain at least one tryptophan.

XX Claim 3; Page 2; 7pp; Japanese.

XX This peptide is a synthetic marker peptide used for isoelectric focusing
CC electrophoresis, particularly capillary isoelectric focusing
CC electrophoresis. The peptide contains at least on tryptophan amino acid
CC residue for detection in the UV absorption range. The markers (AAW78364-
CC W78379) provide sharp isolation, large UV absorption intensity and wide
CC range of pI, and can be easily handled

XX Sequence 6 AA;

Query Match 47.3%; Score 26; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
DB 1 WEYF 4

RESULT 10
ABG79015
ID ABG79015 standard; peptide; 6 AA.
XX
AC ABG79015;
XX
DT 15-NOV-2002 (first entry)

XX
DE
XX
KW
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; thymoma; antigen;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
XX (BAYU) BAYLOR COLLEGE MEDICINE.
PA
XX Wang R;
PI
XX WPI; 2002-627577/67.
DR
XX
XX Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
PT
XX
PS Disclosure; Page 14; 61pp; English.

XX The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for a disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,
CC radiation, chemotherapy or gene therapy. The administration of (I), with,
CC preferably dendritic cell is prior to, subsequent to or concurrent with,
CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention

XX Sequence 6 AA;

Query Match 47.3%; Score 26; DB 5; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
DB 1 WEYF 4

RESULT 11
ABR82656
ID ABR82656 standard; peptide; 6 AA.
XX
AC ABR82656;

```
XX DT 04-DEC-2003 (first entry)
XX DE Immune-modulating peptide #5.
XX KW Immune modulation; formyl peptide receptor; antimicrobial; antibacterial;
XX KW antihistric; antiinflammatory; antidiabetic; nephrotropic; cytostatic;
XX KW osteopathic; vasotropic; gene therapy; FPR.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 6 /note= "C-terminal amide"
XX FT Misc-difference 6 /note= "D-form residue"
XX PN WO2003064447-A2.
XX XX 07-AUG-2003.
XX PD 28-JAN-2003; 2003WO-KR000191.
XX PF 29-JAN-2002; 2002US-035230P.
XX PR (POSC-) POSCO.
XX PA (POST-) POSTECH FOUND.
XX PA (RYUS/) RYU S.
XX PA (SUHP/) SUH P.
XX PA (BAEY/) BAE Y.
XX PA (SONG/) SONG J.
XX PI Ryu S, Suh P, Bae Y, Song J;
XX PI WPI; 2003-646137/61.
XX DR New peptide, useful for preparing composition for treating a disorder
XX PT e.g., rheumatoid arthritis, lung inflammation or cancer.
XX PS Claim 1; Page 9; 57pp; English.
XX CC The invention relates to immune-modulating peptides of the formyl
XX CC receptor family comprising a sequence having 3-6 amino acids. The
XX CC peptides are useful for preparing composition for treating a disorder
XX CC e.g., infection, rheumatoid arthritis, Lyme's arthritis, gout, sepsis
XX CC syndrome, hyperthermia, ulcerative colitis, enterocolitis, osteoporosis,
XX CC periodontal disease, glomerulonephritis, type I insulin dependent
XX CC diabetes mellitus, lung inflammation or cancer. Sequences ABR82652-675
XX CC represent specific examples of the immune-modulating peptides of the
XX CC invention
XX SQ Sequence 6 AA;
    Query Match 47.3%; Score 26; DB 7; Length 6;
    Best Local Similarity 60.0%; Pred. No. 1.8e+06;
    Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 WEYFI 5
DB 1 WEYMV 5
    ||| :
    ||| :
RESULT 12
AAP20184
ID AAP20184 standard; peptide; 9 AA.
XX AC AAP20184;
XX XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 19-AUG-1992 (first entry)
XX DE Sequence of analogue of the gonadotropin releasing factor LRF.
```

```
XX KW Gonadotropin; luteinising hormone releasing factor; contraceptive;
XX KW fertility inhibitor; pregnancy termination; abortion;
XX KW spermatogenesis inhibitor; ovulation; sex hormone.
XX OS Mammalia.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /label= p-Glu
XX FT Misc-difference 6 /label= R-D-Phe
XX FT /note= "R=chloro,dichloro,methyl,nitro,
XX FT acetylamino,methoxy,pentamethyl; Specifically claimed
XX FT when R=4-chloro,3,4-dichloro,4-methyl, 4-methoxy,4-
XX FT nitro,pentamethyl"
XX FT Modified-site 9 /label= Pro-NHET
XX PN EP47079-A.
XX PD 10-MAR-1982.
XX PF 12-AUG-1981; 81EP-00303673.
XX PR 29-AUG-1980; 80US-00182595.
XX PR 01-MAR-1982; 82US-00353237.
XX PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX PI Rivier JEF, Vale WW;
XX PI WPI; 1982-20188E/11.
XX DR Peptide analogues of gonadotropin releasing factor - contg. modified D-
XX PT phenylalanine in 6 position, esp. useful for fertility control.
XX PS Claim 1; Page 17; 19pp; English.
XX CC The peptides of the invention are more potent than LRF in inducing
XX CC secretion of gonadotropins, e.g. with 36-143 times the potency of LRF in
XX CC inducing secretion of luteinising hormone by rat pituitary cells. At high
XX CC doses they can be used to inhibit male and female fertility, terminate
XX CC pregnancy, and inhibit spermatogenesis in males. At low doses they can be
XX CC used to restore fertility and allow timing of ovulation. They can also be
XX CC used to reduce sex hormone levels, e.g. in cases of sex-hormone-dependent
XX CC neoplasma, precocious puberty, endometriosis or dysmenorrhoea. (Updated
XX CC on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct
XX CC OS field.)
XX SQ Sequence 9 AA;
    Query Match 47.3%; Score 26; DB 1; Length 9;
    Best Local Similarity 60.0%; Pred. No. 1.8e+06;
    Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 WEYFI 5
DB 3 WSYFL 7
    ||| :
    ||| :
RESULT 13
AAP30521
ID AAP30521 standard; peptide; 9 AA.
XX AC AAP30521;
XX XX 25-MAR-2003 (revised)
DT 16-AUG-2002 (revised)
DT 14-JUN-1992 (first entry)
XX DE Sequence of luteinising hormone releasing factor (LRF) analogue.
```



```

XX AAY45504;
AC
XX
XX 01-DEC-1999 (first entry)
DT
XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #115.
DE
XX
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX
XX WO9945954-A1.
PN
XX
XX 16-SEP-1999.
PD
XX
XX 13-MAR-1998; 98WO-US005039.
PF
XX
XX 13-MAR-1998; 98WO-US005039.
PR
XX
XX (EPIM-) EPIMUNE INC.
PA
XX
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
PI
XX
XX WPI; 1999-551214/46.
DR
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment and
PT diagnosis of cancers and viral diseases.
PT
XX
XX Claim 1; Page 31; 150pp; English.
PS
XX
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also known
CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
CC (CTLs) which destroy antigen-bearing cells are normally induced by an
CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
CC than the intact foreign antigen itself, and are particularly important in
CC tumour rejection and in fighting viral infections. The peptides are
CC therefore useful therapeutically to treat or prevent viral infections and
CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
CC elicit an immune response in individuals susceptible or otherwise at risk
CC of viral infection or cancer, or used to treat chronic or acute
CC conditions. They are also useful diagnostically, and can be used to
CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
CC patient. The polynucleotides encoding the immunogenic peptides are also
CC useful therapeutically and for immunisation as above
XX
XX
SQ Sequence 9 AA;
Query Match 47.3%; Score 26; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 WEYF 4
Db |::|
2 WQYF 5

```

Search completed: September 16, 2005, 11:53:51
 Job time : 157.333 secs

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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:42:23 ; Search time 77.6667 Seconds
(without alignments)
24.899 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LDNFS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 464945

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1980s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	5	6	ABU62026 Human blo
2	26	100.0	5	8	ADS64548 Human blo
3	26	100.0	10	6	ABU62025 Human blo
4	26	100.0	10	8	ADS64547 Human blo
5	22	84.6	7	2	AAR66795 Mouse syn
6	22	84.6	9	3	RAY79016 Urokinase
7	22	84.6	9	3	AAB10884 Human 9D7
8	22	84.6	10	4	RAM3099 Mycoplasma
9	21	80.8	10	3	AAB23572 Sodium ch
10	20	76.9	6	1	AAP81903 A second
11	20	76.9	7	2	AAW81790 D. vivipa
12	20	76.9	8	5	ABB06417 Beta-secr
13	20	76.9	8	5	ABB06478 Beta-secr
14	20	76.9	8	5	ABB06472 Beta-secr
15	20	76.9	8	5	ABB06471 Beta-secr
16	20	76.9	8	5	ABB06473 Beta-secr
17	20	76.9	8	5	ABP62250 Human imm
18	20	76.9	9	6	ABP75300 Chlamydia
19	20	76.9	9	6	ABP68277 Bacillus
20	20	76.9	10	5	ABP61514 Human KRP
21	19	73.1	5	8	ADM09689 Human pro
22	19	73.1	5	8	ADR70855 Human pro
23	19	73.1	7	4	AAG79264 Peptide w
24	19	73.1	8	2	AAW48039 Immunogen
25	19	73.1	8	3	AAW69946 Human Cyc

ALIGNMENTS

RESULT 1

ABU62026
ID ABU62026 standard; peptide; 5 AA.

XX AC ABU62026;

XX XX 26-AUG-2003 (first entry)

XX DE Human blood coagulation factor Va peptide, L5S.

XX KW Human; blood coagulation factor Va; blood clotting factor Va;
KW KW prothrombinase inhibition; prothrombinase-inhibiting peptide;
KW KW blood clotting disorder; thrombotic disorder; blood clot formation;
KW KW blood vessel obstruction; coronary artery disease; unstable angina;
KW KW valvular heart disease; stroke; blood anticoagulation; anticoagulant.
XX KW atrial fibrillation; stroke; blood anticoagulation; anticoagulant.

XX OS Homo sapiens.

XX PN US2003040600-A1.

XX PD 27-FEB-2003.

XX XX 23-JUL-2001; 2001US-00911129.

XX PR 23-JUL-2001; 2001US-00911129.

XX PA (KALA/) KALAFATIS M. APP.
(MANN/) MANN K.

XX PI Kalafatis M, Mann K;

XX DR WPI; 2003-492177/46.

XX XX Novel anticoagulant peptide derived from the amino acid region 307-356 of human blood clotting factor Va, useful for preventing thrombotic disorders resulting from formation of blood clots that obstruct blood vessels.

XX PS Claim 10; Fig 2; 20pp; English.

XX CC The present invention relates to peptides derived from human blood coagulation (clotting) factor Va which exhibit inhibition of prothrombinase. A pharmaceutical composition comprising one or more of the prothrombinase-inhibiting peptides may be used for treating human subjects with blood clotting disorders. The peptides are useful for preventing thrombotic disorders resulting from the formation of blood clots that obstruct blood vessels, e.g. due to a condition chosen from

CC coronary artery disease, valvular heart disease, stable and unstable
 CC angina, myocardial infarction, atrial fibrillation and stroke. The
 CC peptides of the invention exhibit an IC50 of between 50 nanom-500 microM
 CC for inhibition of prothrombinase. The peptides exhibit excellent blood
 CC anticoagulation properties with little or no adverse side effects. The
 CC present sequence represents a peptide that inhibits prothrombinase
 CC activity

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 LDNFS 5
 Db |||||
 1 LDNFS 5

RESULT 2
 ADS64548
 ID ADS64548 standard; peptide; 5 AA.

XX AC ADS64548;

XX DT 16-DEC-2004 (first entry)

XX DE Human blood coagulation factor Va peptide, L5S.

XX KW Prothrombinase inhibitor; human; blood coagulation factor Va;
 XX blood clotting disorder; thrombotic disorder; thrombolytic.

XX OS Homo sapiens.

XX PN US2004186271-A1.

XX PD 23-SEP-2004.

XX PF 08-MAR-2004; 2004US-00795795.

XX PR 23-JUL-2001; 2001US-00911129.

XX PA (KALA/) KALAFATIS M.

XX PA (MANN/) MANN K G.

XX PI Kalafatis M, Mann KG;

XX DR WPI; 2004-689241/67.

XX PT New prothrombinase-inhibiting peptide derived from a specific amino acid
 PT sequence of human blood coagulation factor Va, useful for treating human
 PT subjects with blood clotting disorders.

XX PS Claim 10; SEQ ID NO 12; 20pp; English.

XX CC The present invention relates to a prothrombinase-inhibiting peptide
 CC derived from a specific amino acid sequence of human blood coagulation
 CC factor Va. The invention is useful for treating human subjects with blood
 CC clotting disorders. The invention is also useful for preventing
 CC thrombotic disorders resulting from formation of blood clots that
 CC obstructs blood vessels. The present sequence is the human blood
 CC coagulation factor Va peptide.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 LDNFS 5
 Db |||||
 1 LDNFS 5

RESULT 3
 ABU62025

ID ABU62025 standard; peptide; 10 AA.

XX AC ABU62025;

XX DT 26-AUG-2003 (first entry)

XX DE Human blood coagulation factor Va peptide, AP9.

XX KW Human; blood coagulation factor Va; blood clotting factor Va;
 XX prothrombinase inhibition; prothrombinase-inhibiting peptide;
 XX blood clotting disorder; thrombotic disorder; blood clot formation;
 KW blood vessel obstruction; coronary artery disease; unstable angina;
 KW valvular heart disease; stable angina; myocardial infarction;
 KW atrial fibrillation; stroke; blood anticoagulation; anticoagulant.

XX OS Homo sapiens.

XX PN US2003040600-A1.

XX PD 27-FEB-2003.

XX PF 23-JUL-2001; 2001US-00911129.

XX PR 23-JUL-2001; 2001US-00911129.

XX PA (KALA/) KALAFATIS M.

XX PA (MANN/) MANN K.

XX PI Kalafatis M, Mann K;

XX DR WPI; 2003-492177/46.

XX PT Novel anticoagulant peptide derived from the amino acid region 307-356 of
 PT human blood clotting factor Va, useful for preventing thrombotic
 PT disorders resulting from formation of blood clots that obstruct blood
 PT vessels.

XX PS Claim 10; Fig 2; 20pp; English.

XX CC The present invention relates to peptides derived from human blood
 CC coagulation (clotting) factor Va which exhibit inhibition of
 CC prothrombinase. A pharmaceutical composition comprising one or more of
 CC the prothrombinase-inhibiting peptides may be used for treating human
 CC subjects with blood clotting disorders. The peptides are useful for
 CC preventing thrombotic disorders resulting from the formation of blood
 CC clots that obstruct blood vessels, e.g. due to a condition chosen from
 CC coronary artery disease, valvular heart disease, stable and unstable
 CC angina, myocardial infarction, atrial fibrillation and stroke. The
 CC peptides of the invention exhibit an IC50 of between 50 nanom-500 microM
 CC for inhibition of prothrombinase. The peptides exhibit excellent blood
 CC anticoagulation properties with little or no adverse side effects. The
 CC present sequence represents a peptide that inhibits prothrombinase
 CC activity

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 26; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5
 Db |||||
 6 LDNFS 10

RESULT 4
 ADS64547

ID ADS64547 standard; peptide; 10 AA.

XX AC ADS64547;

XX 16-DEC-2004 (first entry)
 XX Human blood coagulation factor Va peptide, AP9.
 DE Prothrombinase inhibitor; human; blood coagulation factor Va;
 XX blood clotting disorder; thrombotic disorder; thrombolytic.
 KW Homo sapiens.
 XX OS
 XX US2004186271-A1.
 XX 23-SEP-2004.
 XX 08-MAR-2004; 2004US-00795795.
 XX 23-JUL-2001; 2001US-00911129.
 XX (KALA/) KALAPATIS M.
 XX (MANN/) MANN K G.
 XX Kalafatis M, Mann KG;
 XX WPI; 2004-689241/67.
 XX New prothrombinase-inhibiting peptide derived from a specific amino acid
 PT sequence of human blood coagulation factor Va, useful for treating human
 FT subjects with blood clotting disorders.
 XX Claim 10; SEQ ID NO 11; 20pp; English.
 XX The present invention relates to a prothrombinase-inhibiting peptide
 CC derived from a specific amino acid sequence of human blood coagulation
 CC factor Va. The invention is useful for treating human subjects with blood
 CC clotting disorders. The invention is also useful for preventing
 CC thrombotic disorders resulting from formation of blood clots that
 CC obstructs blood vessels. The present sequence is the human blood
 CC coagulation factor Va peptide.
 XX Sequence 10 AA;
 XX
 XX Query Match 100.0%; Score 26; DB 8; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 22;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LDNFS 5
 Db 6 LDNFS 10
 XX
 XX RESULT 5
 XX AAR66795
 XX AAR66795 standard; peptide; 7 AA.
 XX AC AAR66795;
 XX 25-MAR-2003 (revised)
 XX 11-SEP-1995 (first entry)
 XX Mouse syndecan-1 heparan-attachment site sequence.
 XX Cell surface; proteoglycan; syndecan; mouse; mammary; epithelial cell;
 KW ectodomain; NMuMG; glycosylation; heparan sulphate; chondroitin sulphate;
 KW chimaera; chimaeric molecule; effector molecule; receptor; drug;
 KW antibody; diagnostic agent.
 XX OS Mus musculus.
 XX WO9500633-A2.
 XX 05-JAN-1995.
 XX 17-JUN-1994; 94WO-US006920.

XX 17-JUN-1993; 93US-00078683.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA (STRD) UNIV LEAND STANFORD JUNIOR.
 XX Saunders S, Bernfield M, Kato M;
 XX WPI; 1995-052071/07.
 XX DNA and protein sequences for recombinant syndecan-derived
 PT proteoglycan(s) - comprising a core protein having glycosylation sites
 PT for heparin sulphate glycosaminoglycan side chains.
 XX Claim 4; Page 79; 97pp; English.
 XX The sequence of the heparan sulphate attachment site of the mouse
 CC syndecan-1 protein. The sequence is found at position 45-48 of the
 CC complete syndecan-1 amino acid sequence (AAR66793). The sequence conforms
 CC to the generic attachment site sequence (AAR66794) based on amino acid
 CC sequence comparisons between syndecan 1-4 proteins. The glycosylation
 CC site is found in the extracellular domain of the protein. The functional
 CC domains, esp. the soluble extracellular or heparan binding site, of the
 CC syndecan molecules (see AAR66797-812 and AAR66818) can be used to
 CC construct chimeras by linking them to biological effector molecules,
 CC cell surface receptors, drugs, antibodies, diagnostic agents or
 CC components of microorganisms. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX Sequence 7 AA;
 XX
 XX Query Match 84.6%; Score 22; DB 2; Length 7;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 DNFS 5
 Db 1 DNFS 4
 XX
 XX RESULT 6
 XX AAY79016
 XX ID AAY79016 standard; peptide; 9 AA.
 XX AC AAY79016;
 XX 05-JUN-2000 (first entry)
 XX Urokinase receptor antagonist peptide AE113.
 XX Antagonist; urokinase plasminogen activator; uPA; cancer; plasmin;
 KW myeloid leukaemia; urokinase plasminogen activator receptor; plasminogen;
 KW malignant glioma gastric cancer; proteolysis.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX Misc-difference 4 /note= "D form residue"
 XX Misc-difference 5 /note= "D form residue"
 XX WO200001802-A2.
 XX 13-JAN-2000.
 XX 01-JUL-1999; 99WO-DK000377.
 XX 01-JUL-1998; 98DK-00000874.
 XX (CANC-) CANCERFORSKNINGSFONDET AF 1989.
 XX Ploug M, Ostergaard S, Holm A, Holst-Hansen C, Stephens RW;

match 100%

PI Dano K;
 XX WPI; 2000-171009/15.
 XX
 XX New peptides that antagonize the urokinase receptor, used for treating
 PT cancer by preventing localized conversion of plasminogen to plasmin.
 XX
 XX Disclosure; Page 51; 75pp; English.
 XX
 XX This sequence represents a urokinase receptor (UPAR) antagonist peptide.
 CC The peptide inhibits the binding interaction between human urokinase
 CC plasminogen activator (uPA) and its cell surface receptor (UPAR).
 CC Preventing uPA binding to UPAR, reduces the ability of uPA to convert
 CC plasminogen to plasmin, this results in a reduction of localised
 CC proteolysis caused by plasmin. The peptides of the invention are used to
 CC treat cancer, particularly acute myeloid leukaemia, malignant gliomas and
 CC gastric cancer
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 84.6%; Score 22; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DNFS 5
 DB ||||
 1 DNFS 4
 RESULT 7
 AAB10884
 ID AAB10884 standard; protein; 9 AA.
 XX
 AC AAB10884;
 XX
 DT 26-JAN-2001 (first entry)
 XX
 DE Human 9D7 protein immunogenic fragment SEQ ID NO: 43.
 XX
 XX Tumor-associated antigen; 9D7; human; cytostatic; immunogenic;
 KW immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney;
 KW lung; colon; breast; carcinoma; Hodgkin's lymphoma.
 XX
 XX Homo sapiens.
 XX
 XX DE19909503-A1.
 XX
 XX 07-SEP-2000.
 XX
 XX 04-MAR-1999; 99DE-01009503.
 XX
 XX 04-MAR-1999; 99DE-01009503.
 XX
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX
 PI Klade C, Adolf G, Sommergruber W, Heider K;
 XX WPI; 2000-588357/56.
 XX
 XX New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer
 PT and for producing diagnostic or therapeutic antibodies.
 XX
 XX Claim 6; Page 40; 50pp; German.
 XX
 XX This invention describes a novel tumor-associated antigen, designated 9D7
 CC which has cytostatic activity. The invention also describes a method for
 CC isolating (a) a polypeptide (I) that includes (S) as part of its
 CC sequence; (b) an immunogenic protein fragment or peptide (II) derived
 CC from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7,
 CC (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a
 CC protein (IV) with the immunogenic properties of 9D7 or its fragments; (e)
 CC a recombinant DNA (IIia) that includes (III); and (f) antibodies (Ab)
 CC directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

CC peptides, are used to induce a humoral and/or cellular response for use
 CC in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7
 CC can be used similarly and cells that express 9D7 are useful in cellular
 CC anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for
 CC imaging, diagnosing and monitoring cancers, also, when conjugated to
 CC cytotoxic or radiomucide, as therapeutic agents. Peptides derived from
 CC 9D7 may also be used diagnostically to test for an immune response. 9D7-
 CC associated cancers are particularly kidney, lung, colon and breast
 CC carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic
 CC fragments of the human tumor-associated antigen 9D7 which is described in
 CC the method of the invention
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 84.6%; Score 22; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDNF 4
 DB ||||
 2 LDNF 5
 RESULT 8
 AAM43099
 ID AAM43099 standard; peptide; 10 AA.
 XX
 AC AAM43099;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 408.
 XX
 KW Mycoplasma genitalium; complementary peptide; ligand;
 KW protein-protein interaction; drug design; intermolecular; intramolecular.
 XX
 OS Mycoplasma genitalium.
 XX
 XX WO200142278-A2.
 XX
 XX 14-JUN-2001.
 XX
 XX 13-DEC-2000; 2000WO-GB004778.
 XX
 XX 13-DEC-1999; 99GB-00029466.
 XX
 XX (PROT-) PROTEOM LTD.
 XX
 XX Roberts GW, Heal JR;
 XX
 XX WPI; 2001-514238/56.
 XX
 XX Complementary peptide ligands as reagents and drugs for drug discovery
 PT programs and as lead ligands to facilitate drug design and development,
 PT are generated from microbial genome sequences.
 XX
 XX Example 2; Page 106; 161pp; English.
 XX
 XX The present sequence is one of a large number of complementary peptide
 CC ligands generated from Mycoplasma genitalium genome sequences. These
 CC specific complementary peptides interact with their relevant target
 CC proteins encoded by the microbial genome. They are capable of
 CC antagonising or agonising specific interaction of a protein with another
 CC protein or receptor and are thus useful as reagents and drugs, and as
 CC lead ligands to facilitate drug design and development. They are useful
 CC as tools for functional genomic studies, reagents for the configuration
 CC of high-throughput screens, as a starting point for medicinal chemistry
 CC manipulation, for peptide mimetics and as therapeutic agents. The
 CC analysis and acquisition of peptide sequences facilitates understanding
 CC of protein-protein interactions. The method allows for analysis of an
 CC entire database at a time, thus overcoming sampling problems. The set of
 CC complementary peptides includes both intermolecular (between proteins)
 CC and intermolecular (within a protein) sequences


```

XX SQ Sequence 10 AA;
Query Match      84.6%; Score 22; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
DB 1 DNFS 4

RESULT 9
AAB23572
ID AAB23572 standard; peptide; 10 AA.
XX AC AAB23572;
XX DT 09-JAN-2001 (first entry)
XX DE Sodium channel epitope used to design PCR primer Na-3B.
XX KW Sodium channel 8A; SCN8A; human; excitatory cell.
XX OS Homo sapiens.
XX PN JP2000201684-A.
XX PD 25-JUL-2000.
XX PF 11-JAN-1999; 99JP-00004645.
XX PR 11-JAN-1999; 99JP-00004645.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2000-545978/50.
XX PT New sodium channel SCN8A useful for the elucidation physiological
XX PS mechanism participated by excitatory cells.
XX PS Example; Fig 1; 14pp; Japanese.
XX CC This sequence represents an epitope fragment of various human sodium
XX CC channel proteins. The sequence is used to design a PCR primer, which is
XX CC used in the identification of a human sodium channel SCN8A encoding cDNA
XX CC sequence. The invention provides the SCN8A encoding gene sequence,
XX CC protein sequence, and an antibody against the sodium channel. The SCN8A
XX CC protein alpha subunit and its encoding cDNA can be used in the
XX CC elucidation of the physiological mechanisms of excitatory cells
XX SQ Sequence 10 AA;
Query Match      80.8%; Score 21; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5
DB 5 IDNFS 9

RESULT 10
AAP81903
ID AAP81903 standard; protein; 6 AA.
XX AC AAP81903;
XX DT 25-MAR-2003 (revised)
XX DT 03-OCT-2002 (revised)
XX DT 11-OCT-1990 (first entry)
XX DE A second minor tryptic fragment derived from colon p40 OSN.

XX KW organ specific neoantigen (OSN); lung cancer; colon p40;
XX KW leucocyte adherence inhibition.
XX OS Homo sapiens.
XX PN WO8800344-A.
XX PD 14-JAN-1988.
XX PF 02-JUL-1987; 87WO-US001595.
XX PR 03-JUL-1986; 86US-00881887.
XX PA (BIRA ) BIO RAD LAB INC.
XX PI Walker RP, Lamotte G, Thomson DMP;
XX WPI; 1988-021672/03.
XX PT New peptide fragments reactive with organ specific neoantigen - useful
XX PT in leucocyte adherence inhibition tests for diagnosis and monitoring of
XX PT cancer, and corresp. antibodies.
XX PS Claim 9; Page 50; 62pp; English.
XX CC Peptide was obtained following trypsin digestion of colon p40 OSN. The
XX CC invention covers peptides having at least 80% homology with this peptide.
XX CC See also AAP81585-P81599, AAP81900-2 and AAP81904-5 (Updated on 03-OCT-
XX CC 2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
XX CC field.)
XX SQ Sequence 6 AA;
Query Match      76.9%; Score 20; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFP 4
DB 1 IDNFP 4

RESULT 11
AAW81790
ID AAW81790 standard; peptide; 7 AA.
XX AC AAW81790;
XX DT 27-AUG-2003 (revised)
XX DT 29-JAN-1999 (first entry)
XX DE D. viviparus DV17 antigen Lys C proteolytic peptide fragment #2.
XX KW DV17; antigen; lungworm; immunogenic protein; ELISA; antibody; cattle;
XX KW enzyme linked immunosorbent assay; vaccine; dictyocauliasis.
XX OS Dictyocaulus viviparus.
XX PN DE19715586-A1.
XX PD 22-OCT-1998.
XX PF 15-APR-1997; 97DE-01015586.
XX PR 15-APR-1997; 97DE-01015586.
XX PA (FARH ) HOECHST AG.
XX PI Hofmann J, Schmid K, Pauli A;
XX WPI; 1998-558238/48.
XX DR N-PSDB; AAV64648.

```


Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
:|||
Db 4 MDNF 7

RESULT 14

ABB06472
ID ABB06472 standard; peptide; 8 AA.
XX AC ABB06472;
XX
XX
DT 31-MAY-2002 (first entry)
XX
XX Beta-secretase related peptide SEQ ID NO:66.
DE
XX Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
KW Alzheimer's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200206306-A2.
XX
PD 24-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US023035.
XX
PR 19-JUL-2000; 2000US-0219795P.
PR 12-MAR-2001; 2001US-0275251P.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
PI Heinrichson RL;
PI
XX WPI; 2002-216995/27.
XX
XX Novel substrates for human aspartyl protease useful for identifying
PT modulators of beta secretase activity of aspartyl protease for treating
PT Alzheimer's disease.
XX
XX Disclosure; Page 138; 188pp; English.

The present invention describes an isolated peptide (I) comprising a sequence of at least four amino acids, where the peptide is a substrate for conducting aspartyl protease assays. (I) has neuroprotective and nootropic activities, and can be used as an inhibitor of beta-secretase activity. A beta-secretase modulator from the present invention can be used for inhibiting beta-secretase activity in vivo, and in the manufacture of a medicament for the treatment of Alzheimer's disease. Pharmaceutical compositions from the present invention can be used for treating a disease or condition characterised by an abnormal beta-secretase activity. (I) is useful for identifying agents that modulate the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as a core structure to construct derivatives. ABL49914 to ABL49925 and ABB06409 to ABB06593 represent sequences used in the exemplification of the present invention

Sequence 8 AA;

Query Match 76.9%; Score 20; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
:|||
Db 4 MDNF 7

Search completed: September 16, 2005, 11:53:53
Job time : 79.6667 secs

RESULT 15

ABB06471
ID ABB06471 standard; peptide; 8 AA.
XX
XX AC ABB06471;
XX
XX
DT 31-MAY-2002 (first entry)
XX
XX Beta-secretase related peptide SEQ ID NO:65.
DE
XX Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
KW Alzheimer's disease.
XX
OS Homo sapiens.
OS Synthetic.
XX WO200206306-A2.
XX
PD 24-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US023035.
XX
PR 19-JUL-2000; 2000US-0219795P.
PR 12-MAR-2001; 2001US-0275251P.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
PI Heinrichson RL;
PI
XX WPI; 2002-216995/27.
XX
XX Novel substrates for human aspartyl protease useful for identifying
PT modulators of beta secretase activity of aspartyl protease for treating
PT Alzheimer's disease.
XX
XX Disclosure; Page 138; 188pp; English.

The present invention describes an isolated peptide (I) comprising a sequence of at least four amino acids, where the peptide is a substrate for conducting aspartyl protease assays. (I) has neuroprotective and nootropic activities, and can be used as an inhibitor of beta-secretase activity. A beta-secretase modulator from the present invention can be used for inhibiting beta-secretase activity in vivo, and in the manufacture of a medicament for the treatment of Alzheimer's disease. Pharmaceutical compositions from the present invention can be used for treating a disease or condition characterised by an abnormal beta-secretase activity. (I) is useful for identifying agents that modulate the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as a core structure to construct derivatives. ABL49914 to ABL49925 and ABB06409 to ABB06593 represent sequences used in the exemplification of the present invention

Sequence 8 AA;

Query Match 76.9%; Score 20; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
:|||
Db 4 MDNF 7

Search completed: September 16, 2005, 11:53:53
Job time : 79.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:46:13 ; Search time 15.6667 Seconds
(without alignments)
30.707 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LDNFS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	69.2	7	2 B44787	calliFMRamide 11
2	18	69.2	10	2 C44787	calliFMRamide 12
3	17	65.4	10	2 S27178	neurokinin A-relat
4	16	61.5	8	2 A44960	neuropeptide led-C
5	16	61.5	8	2 A61348	red pigment-concen
6	16	61.5	8	2 S08995	hypertrehalosemic
7	16	61.5	8	2 A49823	adipokinetic hormo
8	16	61.5	8	2 A28004	adipokinetic hormo
9	16	61.5	8	2 A43976	hypertrehalosemic
10	16	61.5	8	2 B43976	hypertrehalosemic
11	16	61.5	8	2 A05169	neuropeptide M-I -
12	16	61.5	9	2 S19523	orf AB protein - S
13	16	61.5	10	2 S08997	hypertrehalosemic
14	16	61.5	10	2 A60421	hypertrehalosemic
15	16	61.5	10	2 S08998	hypertrehalosemic
16	16	61.5	10	2 A26381	hypertrehalosemic
17	16	61.5	10	2 S53789	neuropeptide Pec-H
18	15	57.7	10	2 PN0136	papsin (EC 3.4.23)
19	15	57.7	10	2 P70284	Ig heavy chain CRD
20	14	53.8	10	2 S70251	nitrogenase (EC 1)
21	13	50.0	5	2 P70281	Ig heavy chain CRD
22	13	50.0	8	2 A58620	adipokinetic hormo
23	13	50.0	8	2 S53106	adipokinetic hormo
24	13	50.0	8	2 S10596	adipokinetic hormo
25	13	50.0	8	2 S15422	adipokinetic hormo
26	13	50.0	8	2 A58641	adipokinetic hormo
27	13	50.0	8	2 PL0184	capsid protein vp-
28	13	50.0	8	2 PC4131	hypothetical prote
29	13	50.0	8	2 S11078	glucose-6-phosphat

30	13	50.0	8	2 S21663	neuropeptide - flo
31	13	50.0	8	2 A14683	aspartate transami
32	13	50.0	9	2 PT0315	Ig heavy chain CRD
33	13	50.0	9	2 PT0562	T-cell receptor be
34	13	50.0	9	2 S10784	enamelin i - bovin
35	13	50.0	10	2 JN0024	neurokinin A - chi
36	13	50.0	10	2 A47593	mercury resistance
37	13	50.0	10	2 S18396	probable glucose-6
38	13	50.0	10	2 E44644	neurotoxin-associa
39	13	50.0	10	2 A58365	neuropeptide FFRPa
40	13	50.0	10	2 B61033	ranatachykinin B -
41	12	46.2	4	2 A41890	protein D - Escher
42	12	46.2	4	2 D41654	hypothetical prote
43	12	46.2	6	2 A43129	neuropeptide GNFR
44	12	46.2	7	2 S16364	opacity protein P.
45	12	46.2	7	2 S16365	opacity protein P.

ALIGNMENTS

RESULT 1

B44787

calliFMRamide 11 - bluebottle fly (Calliphora vomitoria)

C;Species: Calliphora vomitoria

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: B44787

R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe,

Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desig

A;Reference number: A41978; MUID:92196111; PMID:1549595

A;Accession: B44787

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <DUV>

A;Cross-references: UNIPROT:P41866

C;Keywords: amidated carboxyl end; neuropeptide

F;7/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 69.2%; Score 18; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4

DB 2 DNF 4

RESULT 2

C44787

calliFMRamide 12 - bluebottle fly (Calliphora vomitoria)

C;Species: Calliphora vomitoria

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: C44787

R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe

Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi

A;Reference number: A41978; MUID:92196111; PMID:1549595

A;Accession: C44787

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <DUV>

A;Cross-references: UNIPROT:P41867

C;Keywords: amidated carboxyl end; neuropeptide

F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 69.2%; Score 18; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4

DB 5 DNF 7

neurokinin A-related peptide - laughing frog
C:Species: Rana ridibunda (laughing frog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C:Accession: S27178
R:Wang, Y.; Badgery-Parker, T.; Lovas, S.; Chartrel, N.; Vaudry, H.; Burcher, E.; Conlon
Biochem. J. 287, 827-832, 1992
A:Title: Primary structure and receptor-binding properties of a neurokinin A-related pep
A:Reference number: S27178; MUID:93075037; PMID:1332583
A:Accession: S27178
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <WAN>
A:Cross-references: UNIPROT:P29135

Query Match 65.4%; Score 17; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNF 4
Db 3 LPSF 6

RESULT 4
A4960
neuropeptide Led-CC-I - Colorado potato beetle
C:Species: Leptinotarsa decemlineata (Colorado potato beetle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: A44960
R:Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A:Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
A:Reference number: A44960; MUID:90160053; PMID:2576128
A:Accession: A44960
A:Molecule type: protein
A:Residues: 1-8 <GAE>
A:Cross-references: UNIPROT:P04548
C:Superfamily: adipokinetic hormone
C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 61.5%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
Db 3 NFS 5

RESULT 5
A61348
red pigment-concentrating hormone - northern shrimp
N:Alternate names: blanching hormone
C:Species: Pandalus borealis (northern shrimp)
C:Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: A61348; S07139
R:Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A:Reference number: A61348; MUID:72228738; PMID:5041363
A:Accession: A61348
A:Molecule type: protein
A:Residues: 1-8 <FER1>
A:Cross-references: UNIPROT:P08939
R:Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus bore

A:Reference number: S07139; MUID:75054965; PMID:4433569
A:Accession: S07139
A:Molecule type: protein
A:Residues: 'E', 2-8 <PER2>
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C:Comment: this neuropeptide, isolated from the eyestalks of the shrimp and active in pig
zed pigment-containing cells.
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 61.5%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
Db 3 NFS 5

RESULT 6
S08995
hypertrehalosemic hormone I - oriental cockroach
N:Alternate names: Pea-CAH-I
C:Species: Blatta orientalis (oriental cockroach)
C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C:Accession: S08995
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S08995
A:Molecule type: protein
A:Residues: 1-8 <GAE>
A:Cross-references: UNIPROT:P04548
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 61.5%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
Db 3 NFS 5

RESULT 7
A49823
adipokinetic hormone I - American cockroach
N:Alternate names: periplanetin CC-1
C:Species: Periplaneta americana (American cockroach)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A49823
R:Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.J.
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hype
A:Reference number: A49823; MUID:84298179; PMID:6591205
A:Accession: A49823
A:Molecule type: protein
A:Residues: 1-8 <SCA>
A:Cross-references: UNIPROT:P04548
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 61.5%; Score 16; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NFS 5
Db 3 NFS 5

RESULT 8
A28004
adipokinetic hormone G - two-spotted cricket
N;Alternate names: AKH-G
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: A28004
R;Gaede, G.; Rinehart, K.L.
Biochem. Biophys. Res. Commun. 149, 908-914, 1987
A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide
A;Reference number: A28004; MUID:88106553; PMID:3426616
A;Accession: A28004
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P14086
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 61.5%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NFS 5
Db 3 NFS 5

RESULT 9
A43976
hypertrehalosemic hormone - yellow mealworm
C;Species: Tenebrio molitor (yellow mealworm)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: A43976
R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle
A;Reference number: A43976; MUID:90341081; PMID:2381871
A;Accession: A43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P25419
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 61.5%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NFS 5
Db 3 NFS 5

RESULT 10
B43976
hypertrehalosemic hormone - beetle (Zophobas rugipes)
C;Species: Zophobas rugipes
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: B43976
R;Gaede, G.; Rosinski, G.

Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle
A;Reference number: A43976; MUID:90341081; PMID:2381871
A;Accession: B43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P25419
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 61.5%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NFS 5
Db 3 NFS 5

RESULT 11
A05169
neuropeptide M-I - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05169
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass
A;Reference number: A90118; MUID:85046530; PMID:6548628
A;Accession: A05169
A;Molecule type: protein
A;Residues: 1-8 <WIT>
A;Cross-references: UNIPROT:P04548
C;Keywords: neuropeptide

Query Match 61.5%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NFS 5
Db 3 NFS 5

RESULT 12
S19523
orf AB protein - Shigella dysenteriae insertion sequence IS911
C;Species: Shigella dysenteriae
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S19523
R;Polard, P.; Prere, M.F.; Chandler, M.; Fayet, O.
J. Mol. Biol. 222, 465-477, 1991
A;Title: Programmed translational frameshifting and initiation at an AUU codon in gene e
A;Reference number: S19523; MUID:92085268; PMID:1660923
A;Accession: S19523
A;Molecule type: protein
A;Residues: 1-9 <POL>
A;Cross-references: UNIPROT:Q9R5R1
C;Genetics:
A;Mobile element: insertion sequence IS911

Query Match 61.5%; Score 16; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NFS 5
Db 5 NFS 7

RESULT 13

S08997

hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)

C;Species: Gromphadorina portentosa

C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004

C;Accession: S08997

R;Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment

A;Reference number: S08995; MUID:90253659; PMID:2340112

A;Accession: S08997

A;Molecule type: protein

A;Residues: 1-10 <GAE>

A;Cross-references: UNIPROT:P10939

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 61.5%; Score 16; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5

DB 3 NFS 5

RESULT 14

A60421

hypertrehalosemic hormone - German cockroach

N;Alternate names: Bld-HrTH

C;Species: Blattella germanica (German cockroach)

C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004

C;Accession: A60421; S09137

R;Veenstra, J.A.; Camps, F.

Neuropeptides 15, 107-109, 1990

A;Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blattella germanica

A;Reference number: A60421; MUID:91179584; PMID:2080017

A;Accession: A60421

A;Molecule type: protein

A;Residues: 1-10 <VEE>

A;Cross-references: UNIPROT:P10939

R;Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment

A;Reference number: S08995; MUID:90253659; PMID:2340112

A;Accession: S09137

A;Molecule type: protein

A;Residues: 1-10 <GAE>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 61.5%; Score 16; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5

DB 3 NFS 5

RESULT 15

S08998

hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004

C;Accession: S08998

R;Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment

A;Reference number: S08995; MUID:90253659; PMID:2340112

A;Accession: S08998

A;Molecule type: protein

A;Residues: 1-10 <GAE>

A;Cross-references: UNIPROT:P10939

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 61.5%; Score 16; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5

DB 3 NFS 5

Search completed: September 16, 2005, 11:58:33

Job time : 15.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:46:13 ; Search time 31.3333 Seconds
(without alignments)
30.707 Million cell updates/sec

Title: US-10-795-795-6
Perfect score: 55
Sequence: 1 WEYFIAAEV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 3
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: Pirl:.*
3: Pirl:.*
4: Pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	36.4	8	A59495	Vesicle associated
2	20	36.4	9	PT0299	Ig heavy chain CRD
3	20	36.4	9	D57444	neuropeptide Grb-A
4	19	34.5	8	S68325	blood cell protein
5	18	32.7	9	A43848	cell surface adhes
6	18	32.7	10	RHPGG	gonadoliberin - pi
7	18	32.7	10	RHSRG	gonadoliberin - sh
8	18	32.7	10	RHAQI	gonadoliberin I -
9	18	32.7	10	A21114	gonadoliberin - ch
10	17	30.9	10	A40753	aldehyde ferredoxi
11	16	29.1	5	PT0308	Ig heavy chain CRD
12	16	29.1	6	S66195	alcohol dehydrogen
13	16	29.1	6	A31263	dihydrofolate redu
14	16	29.1	6	B31263	dihydrofolate redu
15	16	29.1	6	B35640	cerebellar degener
16	16	29.1	8	C61512	variant surface gl
17	16	29.1	8	D61512	variant surface gl
18	16	29.1	8	A59028	MHC class I histoc
19	16	29.1	9	I58350	gene c-mpl protein
20	16	29.1	10	B33995	hypotrehalosemic h
21	16	29.1	10	S59625	beta-galactosidase
22	16	29.1	10	S63696	DNA polymerase - y
23	16	29.1	10	E49033	T-cell receptor ga
24	16	29.1	10	F49033	T-cell receptor ga
25	15	27.3	9	C60070	gastrin - domestic
26	15	27.3	10	S39392	calpain (EC 3.4.22
27	15	27.3	10	PT0215	T-cell receptor be
28	15	27.3	10	S68033	cytochrome P450 1A
29	14	25.5	7	A38081	amine oxidase (cop

30	14	25.5	7	2	S17976	glucose isomerase
31	14	25.5	9	2	D24180	fibrinogen beta ch
32	14	25.5	9	2	S70332	endosperm protein,
33	14	25.5	10	1	SPGNGK	neuromedin K - pig
34	13	23.6	5	2	PT0278	Ig heavy chain CRD
35	13	23.6	5	2	PT0580	T-cell receptor be
36	13	23.6	6	2	PT0519	T-cell receptor be
37	13	23.6	7	2	P80254	18K protein S507 -
38	13	23.6	7	2	S45648	Na+-transporting A
39	13	23.6	7	2	A25269	sex pheromone CAM3
40	13	23.6	8	2	B45800	serum albumin - do
41	13	23.6	8	2	A38887	T-cell receptor ga
42	13	23.6	8	2	B27867	homotetic protein U
43	13	23.6	9	1	AKLQIM	locustamyoinhibiti
44	13	23.6	9	2	D58503	translation elonga
45	13	23.6	9	2	S66608	quinoline 2-oxidor

ALIGNMENTS

RESULT 1

A59495
Vesicle associated membrane protein - Mus musculus
C:Species: Mus musculus
C:Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C:Accession: A59495
R:Bramaraju, M.; Shoen, M.; Laloraya, M.; Kumar, P.
Submitted to the Protein Sequence Database, March 2004
A:Description: Spatio-temporal organization of Vam6P and SNAP on mouse spermatozoa and trafficking through the formation of complexes between proteins present on vesicle and

Query Match 36.4%; Score 20; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEYFIAA 7
DB 2 WEWLLLA 8

RESULT 2

PT0299
Ig heavy chain CRD3 region (clone 5-103B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0299
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

Query Match 36.4%; Score 20; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEY 3
DB 4 WDY 6

```
RESULT 3
D57444
neuropeptide Grb-AST B4 - two-spotted cricket
C:Species: Gryllus bimaculatus (two-spotted cricket)
C>Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
C:Accession: D57444
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
A:Reference number: A57444; MUID:95403341; PMID:7673141
A:Accession: D57444
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LOR>
A:Cross-references: UNIPROT:Q7M3N6

Query Match 36.4%; Score 20; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEYF 4
|||
Db 2 WERF 5

RESULT 4
S68325
blood cell protein A8 - Ascidia ceratodes (fragment)
C:Species: Ascidia ceratodes
C>Date: 13-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: S68325
R:Taylor, S.W.; Ross, M.M.; Waite, J.H.
Arch. Biochem. Biophys. 324, 228-240, 1995
A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from the
A:Reference number: S68325; MUID:96132650; PMID:8554314
A:Accession: S68325
A:Molecule type: protein
A:Residues: 1-8 <TAY>
A:Cross-references: UNIPROT:Q7M3L7
F;2,3,4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental

Query Match 34.5%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EYFIAA 7
|||
Db 1 DYYIAA 6

RESULT 5
A43848
cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)
C:Species: Staphylococcus aureus
C>Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A43848
R:Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
Infect. Immun. 60, 899-906, 1992
A:Title: Binding of heparan sulfate to Staphylococcus aureus.
A:Reference number: A43848; MUID:92176005; PMID:1541563
A:Accession: A43848
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LIA>
A:Cross-references: UNIPROT:Q9R5M1
A>Note: sequence extracted from NCBI backbone (NCBIP:85442)

Query Match 32.7%; Score 18; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEYFIA 7
```

```
Db 2 WTGWLAA 8
|::||
RESULT 6
RHPGG
gonadoliberin - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Mar-1997
C:Accession: A01411
R:Baba, Y.; Mateuo, H.; Schally, A.V.
Biochem. Biophys. Res. Commun. 44, 459-463, 1971
A:Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of the
A:Reference number: A90172; MUID:72114303; PMID:4946067
A:Accession: A01411
A:Molecule type: protein
A:Residues: 1-10 <BAB>
R:Matsumoto, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.
Biochem. Biophys. Res. Commun. 45, 822-827, 1971
A:Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase method
A:Reference number: A90176; MUID:72065376; PMID:4942726
A:Contents: annotation; synthesis
A>Note: the synthetic and natural hormones have the same physicochemical and biological
R:Baba, Y.; Arimura, A.; Schally, A.V.
Biochem. Biophys. Res. Commun. 45, 483-487, 1971
A:Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.
A:Reference number: A90175; MUID:72117544; PMID:4946275
A:Contents: annotation
A>Note: Trp-3 appears to be essential for biological activity
C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and fo
C:Superfamily: gonadoliberin
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 32.7%; Score 18; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3
|||
Db 3 WSY 5

RESULT 7
RHSNG
gonadoliberin - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Mar-1997
C:Accession: A93780; A01411
R:Burgus, R.; Butcher, M.; Amoss, M.; Ling, N.; Monahan, M.; Rivier, J.; Fellows, R.; Bl
Proc. Natl. Acad. Sci. U.S.A. 69, 278-282, 1972
A:Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing factor
A:Reference number: A93780; MUID:72094314; PMID:4550508
A:Accession: A93780
A:Molecule type: protein
A:Residues: 1-10 <BUR>
A>Note: the natural and synthetic hormones have the same biological activity
C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and fo
C:Superfamily: gonadoliberin
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 32.7%; Score 18; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3
|||
Db 3 WSY 5
```

RESULT 8
RHAQ1
Gonadoliberin I - American alligator
N:Alternate names: gonadotropin-releasing hormone I
C:Species: Alligator mississippiensis (American alligator)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: A60066
R:Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson
Regul. Pept. 33, 105-116, 1991
A:Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of
A:Reference number: A60066; MUID:91352338; PMID:1882082
A:Accession: A60066
A:Molecule type: protein
A:Residues: 1-10 <LOV>
A:Cross-references: UNIPROT:P37041
C:Superfamily: gonadoliberin
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 32.7%; Score 18; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3
DB 3 WSY 5

RESULT 9
A21114
gonadoliberin - chum salmon
C:Species: Oncorhynchus keta (chum salmon)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 09-Jul-2004
C:Accession: A21114
R:Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W.
Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983
A:Title: Characterization of a teleost gonadotropin-releasing hormone.
A:Reference number: A21114; MUID:83195140; PMID:6341999
A:Accession: A21114
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SHE>
A:Cross-references: UNIPROT:P20367

Query Match 32.7%; Score 18; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3
DB 3 WSY 5

RESULT 10
A40753
aldehyde ferredoxin oxidoreductase (EC 1.2.7.-) - Pyrococcus furiosus (fragment)
N:Alternate names: glycerolaldehyde:ferredoxin oxidoreductase; red tungsten protein (RTP)
C:Species: Pyrococcus furiosus
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004
C:Accession: A40753
R:Mukund, S.; Adams, M.W.M.
J. Biol. Chem. 266, 14208-14216, 1991
A:Title: The novel tungsten-iron-sulfur protein of the hyperthermophilic archaeobacterium
colytic pathway.
A:Reference number: A40753; MUID:91317766; PMID:1907273
A:Accession: A40753
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <MUK>
A:Cross-references: UNIPROT:Q7M530
C:Keywords: iron-sulfur protein; oxidoreductase; tungsten

Query Match 30.9%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEYFI 5
DB 5 WGRFI 9

RESULT 11
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0308
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0308
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.1%; Score 16; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WE 2
DB 2 WE 3

RESULT 12
S66195
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragment)
C:Species: Gadus sp. (cod)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C:Accession: S66195
R:Hjelmqvist, L.; Hackett, M.; Shafiq, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;
FEBS Lett. 367, 237-240, 1995
A:Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M
nzyme.
A:Reference number: S66191; MUID:95331382; PMID:7607314
A:Accession: S66195
A:Molecule type: protein
A:Residues: 1-6 <HJE>
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 29.1%; Score 16; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WE 2
DB 5 WE 6

RESULT 13
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Welles, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; MUID:89057886; PMID:2904149
A:Accession: A31263
A:Status: not compared with conceptual translation
A:Molecule type: DNA

A;Residues: 1-6 <PET>
C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 29.1%; Score 16; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WE 2
||
Db 3 WE 4

RESULT 14

B31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C;Accession: B31263
R;Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A;Reference number: A94217; MUID:89057886; PMID:2904149
A;Accession: B31263
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-6 <PET>
C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 29.1%; Score 16; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WE 2
||
Db 3 WE 4

RESULT 15

B35640
cerebellar degeneration-related protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
C;Accession: B35640
R;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal marker
A;Reference number: A35640; MUID:90222173; PMID:2326268
A;Accession: B35640
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-6 <CHE>

Query Match 29.1%; Score 16; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WE 2
||
Db 2 WE 3

Search completed: September 16, 2005, 11:58:33
Job time : 33.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:45:28 ; Search time 148 Seconds
(without alignments)
34.600 Million cell updates/sec

Title: US-10-795-795-6
Perfect score: 55
Sequence: 1 WEYFIAABEV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 2547

Minimum DB seq length: 3
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	36.4	8	1 VAM6 MOUSE	P83853 mus musculus
2	20	36.4	9	2 Q7M3N6	Q7m3n6 gryllus bim
3	19	34.5	8	2 Q7M3L7	Q7m3l7 ascidia cer
4	19	34.5	9	2 Q75T44	Q75t44 mus musculus
5	18	32.7	8	2 P79940	P79940 xenopus lae
6	18	32.7	9	2 Q9R5M1	Q9r5m1 staphylococ
7	18	32.7	10	1 GON1 ALLMI	P37041 alligator m
8	18	32.7	10	1 GON3 ONCKE	P20367 oncorhynch
9	17	30.9	8	2 Q7RC74	Q7rc74 plasmodium
10	17	30.9	10	2 Q7M530	Q7m530 pyrococcus
11	17	30.9	10	2 Q93T35	Q93t35 acinetobact
12	16	29.1	8	2 Q7M3S2	Q7m3s2 trypanosoma
13	16	29.1	8	2 Q7M3S3	Q7m3s3 trypanosoma
14	16	29.1	8	2 Q94VC1	Q94vc1 varanus rud
15	16	29.1	8	2 Q70Y57	Q70y57 fuerstia af
16	16	29.1	8	2 Q70Y84	Q70y84 plectranthu
17	16	29.1	8	2 Q9R7T2	Q9r7t2 escherichia
18	16	29.1	9	2 Q9MME4	Q9mmf4 buteo rufin
19	16	29.1	9	2 Q9MME9	Q9mmg9 buteo buteo
20	16	29.1	9	2 Q80X07	Q80x07 mus sp. thr
21	16	29.1	10	1 HTF_TABAT	P14596 tabanus atr
22	16	29.1	10	2 Q8WTT4	Q8wtt4 homo sapien
23	16	29.1	10	2 Q9UC04	Q9ucq4 homo sapien
24	16	29.1	10	2 Q71UL3	Q71ul3 halictis ru
25	15.5	28.2	8	2 Q94VP6	Q94vf6 varanus job
26	15.5	28.2	10	1 GON1 CHEPR	P80677 chelyosoma
27	15	27.3	8	2 Q6BC29	Q6bc29 homo sapien
28	15	27.3	9	1 NEUX CAVPO	P34966 cavia porce
29	15	27.3	9	1 NEUX HUMAN	P04277 homo sapien
30	15	27.3	9	2 Q93LE4	Q93le4 heliobacill
31	15	27.3	9	2 Q85710	Q85710 rous sarcom

32	15	27.3	10	2 Q7SA62	Q7sa62 neurospora
33	15	27.3	10	2 Q7RSI4	Q7rsi4 plasmodium
34	15	27.3	10	2 Q7OF01	Q7of01 sus scrofa
35	15	27.3	10	2 P96305	P96305 alteromonas
36	15	27.3	10	2 P96306	P96306 aeromonas a
37	15	27.3	10	2 P96321	P96321 escherichia
38	15	27.3	10	2 P96352	P96352 marinobacte
39	15	27.3	10	2 P96421	P96421 neisseria g
40	15	27.3	10	2 Q93LES	Q93le5 photobacter
41	15	27.3	10	2 P96423	P96423 pseudomonas
42	15	27.3	10	2 O42355	O42355 brachydanio
43	14	25.5	5	1 RE21_LITRU	P82071 litoria rub
44	14	25.5	5	1 RE31_LITRU	P82072 litoria rub
45	14	25.5	8	2 Q42507	Q42507 triticum ae

ALIGNMENTS

RESULT 1
VAM6 MOUSE STANDARD; PRT; 8 AA.
ID VAM6 MOUSE
AC P83853;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vam6-like protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Sperm;
RA Brahmajulu M., Shueb M., Laloraya M., Kumar G.P.;
RT "Spatio-temporal organization of Vam6P and SNAP on mouse spermatozoa
and their involvement in sperm-zona pellucida interactions.";
RL Submitted (MAR-2004) to Swiss-Prot.
CC -!- FUNCTION: May play a role in clustering and fusion of late
endosomes and lysosomes (By similarity).
CC -!- SUBUNIT: Homooligomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and associated with the
membranes of lysosomes and late endosomes (By similarity).
KW Direct protein sequencing; Protein transport; Transport.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1075 MW; 2CD727337B1B037B CRC64;

Query Match 36.4%; Score 20; DB 1; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEYFIAA 7
|| : : |
Db 2 WEEWLLA 8

RESULT 2
Q7M3N6 PRELIMINARY; PRT; 9 AA.
ID Q7M3N6
AC Q7M3N6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Neuropeptide Grb-AST B4.
OS Gryllus bimaculatus (Two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999;
RN [1]
RP SEQUENCE.
RX MEDLINE=95403341; PubMed=7673141; DOI=10.1074/jbc.270.36.21103;
RA Lorenz M.W., Kellner R., Hoffmann K.H.;

RT "A family of neuropeptides that inhibit juvenile hormone biosynthesis
in the cricket, Gryllus bimaculatus.";
RL J. Biol. Chem. 270:21103-21108(1995).
DR PIR; D57444; D57444.
SQ SEQUENCE 9 AA; 1175 MW; 3860B871E9D40B03 CRC64;

Query Match 36.4%; Score 20; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEYF 4
|||
Db 2 WERF 5

RESULT 3

ID Q7M3L7 PRELIMINARY; PRT; 8 AA.

AC Q7M3L7; DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Blood cell protein A8 (Fragment).

OS Ascidia ceratodes.

OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

OC Phlebobranchia; Ascidiidae; Ascidia.

OX NCBI_TaxID=30276;

RN [1]

RP SEQUENCE.

RX MEDLINE=96132650; PubMed=8554314; DOI=10.1006/abbi.1995.0035;

RA Taylor S.W., Ross M.M., Waite J.H.;

RT "Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing

RT polypeptides from the blood cells of the ascidians Ascidia ceratodes

RT and Molgula manhattensis.";

RL Arch. Biochem. Biophys. 324:228-240(1995).

DR PIR; S68325; S68325.

FT NON_TER 1 1

FT NON_TER 8 8

SQ SEQUENCE 8 AA; 907 MW; D9DDDDDCB4B5A CRC64;

Query Match 34.5%; Score 19; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.6e+06;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EYFIAA 7

:|:|

Db 1 DYYVAA 6

RESULT 4

ID Q75T44

AC Q75T44 PRELIMINARY; PRT; 9 AA.

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Nuclear receptor RORalpha4 (Fragment).

GN Names=RORa4;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Miki N., Ikuta M., Matsui T.;

RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB127583; BAD14939.1; --

DR GO; GO:0004872; F:receptor activity; IEA.

KW Receptor.

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1073 MW; 110F9DDDD042C9DB CRC64;

Query Match 34.5%; Score 19; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 1.6e+06;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YFIAA 7

||:|

Db 2 YFVIA 6

RESULT 5

P79940

ID P79940 PRELIMINARY; PRT; 8 AA.

AC P79940;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE XMeisl-4 protein (Fragment).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97202105; PubMed=9049632;

RA Steelman S., Moskow J.J., Muzynski K., North C., Druck T.,

RA Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.;

RT "Identification of a conserved family of Meisl-related homeobox

RT genes.";

RL Genome Res. 7:142-156(1997).

DR EMBL; U68389; AAB19199.1; --

DR TRANSFAC; T03410; --

FT NON_TER 1 1

SQ SEQUENCE 8 AA; 1187 MW; 278B51F37B11F40B CRC64;

Query Match 32.7%; Score 18; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3

|||

Db 5 WHY 7

RESULT 6

Q9R5M1

ID Q9R5M1 PRELIMINARY; PRT; 9 AA.

AC Q9R5M1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE 66 kDa cell surface adhesin for heparan sulfate (Fragment).

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1280;

RN [1]

RP SEQUENCE.

RX MEDLINE=92176005; PubMed=1541563;

RA Liang O.D., Ascencio F., Fransson L.A., Wadstrom T.;

RT "Binding of heparan sulfate to Staphylococcus aureus.";

RL Infect. Immun. 60:899-906(1992).

DR PIR; A43848; A43848.

FT NON_TER 1 1

FT NON_TER 9 9

SQ SEQUENCE 9 AA; 990 MW; 2289DDDD7337861B3 CRC64;

Query Match 32.7%; Score 18; DB 2; Length 9;

Best Local Similarity 42.9%; Pred. No. 1.6e+06;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEYFIAA 7

||:|

Db 2 WTGWLAA 8

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RESULT 7
CON1_ALLMI STANDARD; PRT; 10 AA.
AC P37041; P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)
DE (uliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1892082; DOI=10.1016/0167-0115(91)90206-V;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone from
RL brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the GnRH family.
DR PIR; A60066; RHAQ1.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Amidation; Direct protein sequencing; Hormone; Hypothalamus;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 10 10 Glycine amide.
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 32.7%; Score 18; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 2e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3
DB 3 WSY 5

RESULT 9
Q7RC74 PRELIMINARY; PRT; 8 AA.
AC Q7RC74;
DT 01-WAR-2004 (TREMELrel. 26, Created)
DT 01-WAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY05910;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABL01001938; EAA18015.1; -.
DR Hypothetical protein.
KW NON_TER 8
SQ SEQUENCE 8 AA; 990 MW; F959DB41B2CEB446 CRC64;

Query Match 30.9%; Score 17; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFI 5
DB 6 YFI 8

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RESULT 10
Q7M530
ID Q7M530 PRELIMINARY; PRT; 10 AA.
AC Q7M530;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DE Aldehyde ferredoxin oxidoreductase (EC 1.2.7.-) (Fragment).
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE.
RX MEDLINE=91317766; PubMed=1907273;
RA Mukund S., Adams M.W.W.;
RT "The novel tungsten-iron-sulfur protein of the hyperthermophilic
archaeobacterium, Pyrococcus furiosus, is an aldehyde ferredoxin
oxidoreductase. Evidence for its participation in a unique glycolytic
pathway."
RL J. Biol. Chem. 266:14208-14216(1991).
DR PIR; A40753; A40753.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1272 MW; 353260D408637448 CRC64;

Query Match 30.9%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.1e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEYFI 5
DB 5 WGRFI 9

RESULT 11
Q93735
ID Q93735 PRELIMINARY; PRT; 10 AA.
AC Q93735;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE Quaternary ammonium compound-resistance protein (Fragment).
GN Name=qacEdelta1;
OS Acinetobacter genomosp. 3.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=48296;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YMCU160;
RX MEDLINE=2199242; PubMed=12003980;
RA Yum J.H., Yi K., Lee H., Yong D., Lee K., Kim J.M., Rossolini G.M.,
Chong Y.;
RT "Molecular characterization of metallo-b-lactamase-producing
Acinetobacter baumannii and Acinetobacter genomosp. 3 from Korea:
identification of two new integrons carrying the bla(VIM-2) gene
cassettes."
RL J. Antimicrob. Chemother. 49:837-840(2002).
DR EMBL; AF369871; AAK54205.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1178 MW; 28287BC729C73378 CRC64;

Query Match 30.9%; Score 17; DB 2; Length 10;
Best Local Similarity 28.6%; Pred. No. 3.1e+04;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEYFIAA 7
DB 4 WLFVLVIA 10

RESULT 12

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Q7M3S2
ID Q7M3S2 PRELIMINARY; PRT; 8 AA.
AC Q7M3S2;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DE Variant surface glycoprotein MITat 1.6 (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE.
RX MEDLINE=81172836; PubMed=6163983; DOI=10.1016/0166-6851(81)90095-5;
RA Holder A.A., Cross G.A.M.;
RT "Glycopeptides from variant surface glycoproteins of Trypanosoma
brucei. C-terminal location of antigenically cross-reacting
carbohydrate moieties."
RL Mol. Biochem. Parasitol. 2:135-150(1981).
DR PIR; D61512; D61512.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 967 MW; 74033EALAB187B03 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WE 2
DB 1 WE 2

RESULT 13
Q7M3S3
ID Q7M3S3 PRELIMINARY; PRT; 8 AA.
AC Q7M3S3;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DE Variant surface glycoprotein MITat 1.4 (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE.
RX MEDLINE=81172836; PubMed=6163983; DOI=10.1016/0166-6851(81)90095-5;
RA Holder A.A., Cross G.A.M.;
RT "Glycopeptides from variant surface glycoproteins of Trypanosoma
brucei. C-terminal location of antigenically cross-reacting
carbohydrate moieties."
RL Mol. Biochem. Parasitol. 2:135-150(1981).
DR PIR; C61512; C61512.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 979 MW; 74033EBDD444B03 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WE 2
DB 1 WE 2

RESULT 14
Q94VC1
ID Q94VC1 PRELIMINARY; PRT; 8 AA.
AC Q94VC1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).

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GN Name=COI;
OS Varanus rudicollis (Rough-necked monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Anguilliformes; Varanidae; Varanus.
OX NCBI_TaxID=169851;
RN [1]_
RP SEQUENCE FROM N.A.
RA Act J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:211-226(2001).
DR EMBL; AF407521; AAL10116.1; -
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1053 MW; FE2729D5A36411A6 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 8;
Best Local Similarity 20.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEYFI 5
DB 4 WSEFL 8

RESULT 15
Q70Y57
ID Q70Y57 PRELIMINARY; PRT; 8 AA.
AC Q70Y57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (fragment).
GN Name=rs16;
OS Eukaryota;
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fierstia.
OX NCBI_TaxID=204226;
RN [1]_
RP SEQUENCE FROM N.A.
RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simmonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 916 MW; DABAB58637041B5 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3
DB 4 WGY 6

```

Search completed: September 16, 2005, 11:57:40
 Job time : 150 secs

This Page Blank (user)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:54:04 ; Search time 65.3333 Seconds
(without alignments)
25.020 Million cell updates/sec

Title: US-10-795-795-6

Perfect score: 55

Sequence: 1 WEYFAAEV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 760079 seqs, 163465437 residues

Total number of hits satisfying chosen parameters: 87311

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:

1: /cgn2_6/prodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/prodata/2/paa/US05_NEW_COMB.pep.*
3: /cgn2_6/prodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/prodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/prodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/prodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	6	7	US-11-043-020-9
2	26	47.3	9	6	US-10-817-970-4124
3	26	47.3	9	6	US-10-817-970-4125
4	26	47.3	9	6	US-10-817-970-4137
5	26	47.3	9	6	US-10-538-066-336
6	26	47.3	9	7	US-11-097-912-101
7	26	47.3	9	7	US-11-097-912-372
8	26	47.3	9	7	US-11-097-912-657
9	26	47.3	9	7	US-11-097-864-101
10	26	47.3	9	7	US-11-097-864-372
11	26	47.3	9	7	US-11-097-864-657
12	26	47.3	10	6	US-10-817-970-4176
13	26	47.3	10	6	US-10-817-970-4177
14	26	47.3	10	6	US-10-817-970-4192
15	26	47.3	10	6	US-10-817-970-4308
16	26	47.3	10	7	US-11-097-912-151
17	26	47.3	10	7	US-11-097-912-207
18	26	47.3	10	7	US-11-097-912-421
19	26	47.3	10	7	US-11-097-912-545
20	26	47.3	10	7	US-11-097-912-637
21	26	47.3	10	7	US-11-097-864-151
22	26	47.3	10	7	US-11-097-864-207
23	26	47.3	10	7	US-11-097-864-421
24	26	47.3	10	7	US-11-097-864-545
25	26	47.3	10	7	US-11-097-864-637

26 25 45.5 8 6 US-10-998-519-6 Sequence 6, Appli
27 25 45.5 8 6 US-10-820-067A-200 Sequence 200, App
28 25 45.5 9 1 PCT-US04-33942-110 Sequence 110, App
29 24 43.6 4 6 US-10-351-641B-1565 Sequence 1565, Ap
30 24 43.6 5 6 US-10-351-641B-1566 Sequence 1566, Ap
31 24 43.6 6 6 US-10-351-641B-1567 Sequence 1567, Ap
32 24 43.6 6 6 US-10-351-641B-1583 Sequence 1583, Ap
33 24 43.6 6 6 US-10-351-641B-1586 Sequence 1586, Ap
34 24 43.6 6 6 US-10-351-641B-1433 Sequence 1433, Ap
35 24 43.6 8 6 US-10-351-641B-1563 Sequence 1563, Ap
36 24 43.6 8 6 US-10-351-641B-1570 Sequence 1570, Ap
37 24 43.6 8 6 US-10-351-641B-1571 Sequence 1571, Ap
38 24 43.6 8 6 US-10-351-641B-1629 Sequence 1629, Ap
39 24 43.6 9 1 PCT-US04-33939-463 Sequence 463, App
40 24 43.6 9 6 US-10-351-641B-1564 Sequence 1564, Ap
41 24 43.6 10 6 US-10-351-641B-1572 Sequence 1572, Ap
42 24 43.6 10 6 US-10-351-641B-1573 Sequence 1573, Ap
43 24 43.6 10 6 US-10-351-641B-1584 Sequence 1584, Ap
44 24 43.6 10 6 US-10-351-641B-1585 Sequence 1585, Ap
45 24 43.6 10 7 US-11-129-260-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-11-043-020-9
; Sequence 9, Application US/11043020
; GENERAL INFORMATION:
; APPLICANT: Premack, Brett
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF W-PEPTIDES
; FILE REFERENCE: 10709/103
; CURRENT APPLICATION NUMBER: US/11/043,020
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: US 60/539,665
; PRIOR FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: W-tide
; NAME/KEY: MOD RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: D-Met
US-11-043-020-9

Query Match 47.3%; Score 26; DB 7; Length 6;
Best Local Similarity 60.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEYFI 5
||| :
Db 1 WEYV 5

RESULT 2
US-10-817-970-4124
; Sequence 4124, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celles, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses

```
; FILE REFERENCE: 2060.0500000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4124
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-4124
```

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Query Match 47.3%; Score 26; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 WEYF 4
|:|
Db 6 WQYF 9
```

```
RESULT 3
US-10-817-970-4125
; Sequence 4125, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.0500000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
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```
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-4125
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Query Match 47.3%; Score 26; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 WEYF 4
|:|
Db 5 WQYF 8
```

```
RESULT 4
US-10-817-970-4137
; Sequence 4137, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.0500000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4137
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-4137
```

```
Query Match          47.3%; Score 26; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEYF 4
Db      2 WQYF 5

RESULT 5
US-10-538-066-336
; Sequence 336, Application US/10538066
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 336
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-336

Query Match          47.3%; Score 26; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEYF 4
Db      2 WQYF 5

RESULT 6
US-11-097-912-101
; Sequence 101, Application US/11097912
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-101

Query Match          47.3%; Score 26; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEYF 4
Db      3 WQYF 6

RESULT 7
US-11-097-912-372
; Sequence 372, Application US/11097912
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-372

Query Match          47.3%; Score 26; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEYF 4
Db      6 WQYF 9

RESULT 8
US-11-097-912-657
; Sequence 657, Application US/11097912
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 657
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-657

Query Match          47.3%; Score 26; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEYF 4
Db      3 WQYF 6
```

```
RESULT 9
US-11-097-864-101
; Sequence 101, Application US/11097864
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faries, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-101

Query Match      47.3%; Score 26; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
        |:|
Db      3 WDYF 6

RESULT 10
US-11-097-864-372
; Sequence 372, Application US/11097864
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faries, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-372

Query Match      47.3%; Score 26; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
        |:|
Db      3 WDYF 6

RESULT 11
US-11-097-864-101
; Sequence 101, Application US/11097864
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faries, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-101

Query Match      47.3%; Score 26; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
        |:|
Db      6 WDYF 9

RESULT 12
US-10-817-970-4176
; Sequence 4176, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.050000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
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SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4176
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic Peptide
 US-10-817-970-4176

Query Match 47.3%; Score 26; DB 6; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
 Db 7 WQYF 10

RESULT 13

US-10-817-970-4177
 ; Sequence 4177, Application US/10817970
 ; GENERAL INFORMATION:
 ; APPLICANT: Grey, H.
 ; APPLICANT: Sette, A.
 ; APPLICANT: Sidney, J.
 ; APPLICANT: Southwood, S.
 ; APPLICANT: Kubo, R.
 ; APPLICANT: Celis, E.
 ; APPLICANT: Chesnut, R.
 ; APPLICANT: Kast, W.M.
 ; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
 ; FILE REFERENCE: 2060.0500000
 ; CURRENT APPLICATION NUMBER: US/10/817,970
 ; CURRENT FILING DATE: 2004-04-06
 ; PRIOR APPLICATION NUMBER: 08/821,739
 ; PRIOR FILING DATE: 1997-03-20
 ; PRIOR APPLICATION NUMBER: 60/013,833
 ; PRIOR FILING DATE: 1996-03-21
 ; PRIOR APPLICATION NUMBER: 08/589,107
 ; PRIOR FILING DATE: 1996-01-23
 ; PRIOR APPLICATION NUMBER: 08/451,913
 ; PRIOR FILING DATE: 1995-05-26
 ; PRIOR APPLICATION NUMBER: 08/186,266
 ; PRIOR FILING DATE: 1994-01-25
 ; PRIOR APPLICATION NUMBER: 08/159,339
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: 08/103,396
 ; PRIOR FILING DATE: 1993-08-06
 ; PRIOR APPLICATION NUMBER: 08/027,746
 ; PRIOR FILING DATE: 1993-03-05
 ; PRIOR APPLICATION NUMBER: 07/926,666
 ; PRIOR FILING DATE: 1992-08-07
 ; PRIOR APPLICATION NUMBER: 08/347,610
 ; PRIOR FILING DATE: 1994-12-01
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 14635
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4177
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Peptide
 US-10-817-970-4177

Query Match 47.3%; Score 26; DB 6; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
 Db 6 WQYF 9

RESULT 14
 US-10-817-970-4192
 ; Sequence 4192, Application US/10817970
 ; GENERAL INFORMATION:
 ; APPLICANT: Grey, H.
 ; APPLICANT: Sette, A.
 ; APPLICANT: Sidney, J.
 ; APPLICANT: Southwood, S.
 ; APPLICANT: Kubo, R.
 ; APPLICANT: Celis, E.
 ; APPLICANT: Chesnut, R.
 ; APPLICANT: Kast, W.M.
 ; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
 ; FILE REFERENCE: 2060.0500000
 ; CURRENT APPLICATION NUMBER: US/10/817,970
 ; CURRENT FILING DATE: 2004-04-06
 ; PRIOR APPLICATION NUMBER: 08/821,739
 ; PRIOR FILING DATE: 1997-03-20
 ; PRIOR APPLICATION NUMBER: 60/013,833
 ; PRIOR FILING DATE: 1996-03-21
 ; PRIOR APPLICATION NUMBER: 08/589,107
 ; PRIOR FILING DATE: 1996-01-23
 ; PRIOR APPLICATION NUMBER: 08/451,913
 ; PRIOR FILING DATE: 1995-05-26
 ; PRIOR APPLICATION NUMBER: 08/186,266
 ; PRIOR FILING DATE: 1994-01-25
 ; PRIOR APPLICATION NUMBER: 08/159,339
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: 08/103,396
 ; PRIOR FILING DATE: 1993-08-06
 ; PRIOR APPLICATION NUMBER: 08/027,746
 ; PRIOR FILING DATE: 1993-03-05
 ; PRIOR APPLICATION NUMBER: 07/926,666
 ; PRIOR FILING DATE: 1992-08-07
 ; PRIOR APPLICATION NUMBER: 08/347,610
 ; PRIOR FILING DATE: 1994-12-01
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 14635
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4192
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Peptide
 US-10-817-970-4192

Query Match 47.3%; Score 26; DB 6; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
 Db 2 WQYF 5

RESULT 15

US-10-817-970-4308
 ; Sequence 4308, Application US/10817970
 ; GENERAL INFORMATION:
 ; APPLICANT: Grey, H.
 ; APPLICANT: Sette, A.
 ; APPLICANT: Sidney, J.
 ; APPLICANT: Southwood, S.
 ; APPLICANT: Kubo, R.
 ; APPLICANT: Celis, E.
 ; APPLICANT: Chesnut, R.
 ; APPLICANT: Kast, W.M.
 ; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
 ; FILE REFERENCE: 2060.0500000
 ; CURRENT APPLICATION NUMBER: US/10/817,970
 ; CURRENT FILING DATE: 2004-04-06

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; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4308
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-4308

Query Match      47.3%; Score 26; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. NO. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WEYF 4
Db      7 WQYF 10

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Search completed: September 16, 2005, 12:12:32
Job time : 66.3333 secs

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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:49:59 ; Search time 444 Seconds
(without alignments)
26.306 Million cell updates/sec

Title: US-10-795-795-6
Perfect score: 55
Sequence: 1 WYFIAAEV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues
Total number of hits satisfying chosen parameters: 755392

Minimum DB seq length: 3
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	55	100.0	10	33	US-10-795-795-6	Sequence 6, Appl
2	44	80.0	9	1	PCT-US04-21487A-24	Sequence 24, Appl
3	33	60.0	10	33	US-10-795-795-5	Sequence 5, Appl
4	27	49.1	10	35	US-10-937-912-105	Sequence 105, App
5	26	47.3	5	1	PCT-US04-21487A-25	Sequence 25, Appl
6	26	47.3	6	29	US-10-353-419A-5	Sequence 5, Appl
7	26	47.3	8	18	US-09-458-298-78	Sequence 78, Appl
8	26	47.3	8	18	US-09-458-298-454	Sequence 454, App
9	26	47.3	8	18	US-09-458-298-772	Sequence 772, App
10	26	47.3	8	18	US-09-458-298-1276	Sequence 1276, Ap
11	26	47.3	8	18	US-09-458-298-1279	Sequence 1279, Ap
12	26	47.3	8	18	US-09-458-298-1654	Sequence 1654, Ap
13	26	47.3	8	18	US-09-458-298-1658	Sequence 1658, Ap
14	26	47.3	8	18	US-09-458-298A-78	Sequence 78, Appl
15	26	47.3	8	18	US-09-458-298A-454	Sequence 454, App
16	26	47.3	8	18	US-09-458-298A-772	Sequence 772, App
17	26	47.3	8	18	US-09-458-298A-1276	Sequence 1276, Ap
18	26	47.3	8	18	US-09-458-298A-1279	Sequence 1279, Ap
19	26	47.3	8	18	US-09-458-298A-1654	Sequence 1654, Ap
20	26	47.3	8	18	US-09-458-298A-1658	Sequence 1658, Ap
21	26	47.3	8	18	US-09-458-298B-78	Sequence 78, Appl
22	26	47.3	8	18	US-09-458-298B-454	Sequence 454, App
23	26	47.3	8	18	US-09-458-298B-772	Sequence 772, App
24	26	47.3	8	18	US-09-458-298B-1276	Sequence 1276, Ap
25	26	47.3	8	18	US-09-458-298B-1279	Sequence 1279, Ap
26	26	47.3	8	18	US-09-458-298B-1654	Sequence 1654, Ap
27	26	47.3	8	18	US-09-458-298B-1658	Sequence 1658, Ap
28	26	47.3	8	27	US-10-149-135-78	Sequence 78, Appl
29	26	47.3	8	27	US-10-149-135-454	Sequence 454, App
30	26	47.3	8	27	US-10-149-135-772	Sequence 772, App
31	26	47.3	8	27	US-10-149-135-1276	Sequence 1276, Ap
32	26	47.3	8	27	US-10-149-135-1279	Sequence 1279, Ap
33	26	47.3	8	27	US-10-149-135-1654	Sequence 1654, Ap
34	26	47.3	8	27	US-10-149-135-1658	Sequence 1658, Ap
35	26	47.3	9	1	PCT-US03-10571-116	Sequence 116, App
36	26	47.3	9	1	PCT-US03-16736-26	Sequence 26, Appl
37	26	47.3	9	1	PCT-US03-38949-336	Sequence 336, App
38	26	47.3	9	7	US-08-347-610-186	Sequence 186, App
39	26	47.3	9	7	US-08-347-610-187	Sequence 187, App
40	26	47.3	9	7	US-08-347-610-199	Sequence 199, App
41	26	47.3	9	7	US-08-347-610A-186	Sequence 186, App
42	26	47.3	9	7	US-08-347-610A-187	Sequence 187, App
43	26	47.3	9	7	US-08-347-610A-199	Sequence 199, App
44	26	47.3	9	7	US-08-347-610B-186	Sequence 186, App
45	26	47.3	9	7	US-08-347-610B-187	Sequence 187, App

ALIGNMENTS

RESULT 1
US-10-795-795-6
; Sequence 6, Application US/10795795
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795, 795
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-795-795-6
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Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYFIAAEV 10
Db 1 WEYFIAAEV 10

RESULT 2
PCT-US04-21487A-24
; Sequence 24, Application PC/TUS0421487A
; GENERAL INFORMATION:
; APPLICANT: Kalafatis, Michael
; TITLE OF INVENTION: EXOSITE-DIRECTED THROMBIN INHIBITORS
; FILE REFERENCE: CLEV 200023
; CURRENT APPLICATION NUMBER: PCT/US04/21487A
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US 60/502,186
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-21487A-24

Query Match      80.0%; Score 44; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYFIAAEV 10
Db 1 EYFIAAEV 9

RESULT 3
US-10-795-795-5
; Sequence 5, Application US/10795795
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-795-795-5

Query Match      60.0%; Score 33; DB 33; Length 10;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYFI 5
Db 6 WEYFI 10

RESULT 4
US-10-937-912-105
; Sequence 105, Application US/10937912
; GENERAL INFORMATION:
; APPLICANT: Baxter International Inc.
; APPLICANT: Johnson, Richard J
; APPLICANT: Maves, Shelley A
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT COMPLEMENT ACTIVATION
; FILE REFERENCE: TR-6067 (BXTR 4017.1)
; CURRENT APPLICATION NUMBER: US/10/937,912
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/501,710
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: complement inhibitor
US-10-937-912-105

Query Match      49.1%; Score 27; DB 35; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYFI 5
Db 6 WEYFI 10

RESULT 5
PCT-US04-21487A-25
; Sequence 25, Application PC/TUS0421487A
; GENERAL INFORMATION:
; APPLICANT: Kalafatis, Michael
; TITLE OF INVENTION: EXOSITE-DIRECTED THROMBIN INHIBITORS
; FILE REFERENCE: CLEV 200023
; CURRENT APPLICATION NUMBER: PCT/US04/21487A
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US 60/502,186
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-21487A-25

Query Match      47.3%; Score 26; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYFIA 6
Db 1 EYFIA 5

RESULT 6
US-10-353-419A-5
; Sequence 5, Application US/10353419A
; GENERAL INFORMATION:
; APPLICANT: Ryu, Sung-ho
; APPLICANT: Suh, Pann-Chill
; APPLICANT: Bae, Yoe-Sik
; APPLICANT: Song, Ji-Young
; TITLE OF INVENTION: Immune Modulating Peptides
; FILE REFERENCE: AP34977 072944.0167
; CURRENT APPLICATION NUMBER: US/10/353,419A
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/352,930
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
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; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immune-modulating peptide
; NAME/KEY: MOD_RES
; LOCATION: 6
; OTHER INFORMATION: D-Met
US-10-353-419A-5

Query Match 47.3%; Score 26; DB 29; Length 6;
Best Local Similarity 60.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEYF 5
||| :
Db 1 WEYV 5

RESULT 7
US-09-458-298-78

; Sequence 78, Application US/09458298
; GENERAL INFORMATION:
; APPLICANT: Epimmune
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO
; FILE REFERENCE: 018623-014600US
; CURRENT APPLICATION NUMBER: US/09/458,298
; CURRENT FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2436
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-458-298-78

Query Match 47.3%; Score 26; DB 18; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
||| :
Db 5 WQYF 8

RESULT 8
US-09-458-298-454
; Sequence 454, Application US/09458298
; GENERAL INFORMATION:
; APPLICANT: Epimmune
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO
; FILE REFERENCE: 018623-014600US
; CURRENT APPLICATION NUMBER: US/09/458,298
; CURRENT FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2436
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 454
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-458-298-454

Query Match 47.3%; Score 26; DB 18; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
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Db 1 WQYF 4

RESULT 9

US-09-458-298-772
; Sequence 772, Application US/09458298
; GENERAL INFORMATION:
; APPLICANT: Epimmune
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO
; FILE REFERENCE: 018623-014600US
; CURRENT APPLICATION NUMBER: US/09/458,298
; CURRENT FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2436
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 772
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:


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Db          |:||
            4 WQYF 7

RESULT 13
US-09-458-298-1658
; Sequence 1658, Application US/09458298
; GENERAL INFORMATION:
; APPLICANT: Epimmune
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO
; FILE REFERENCE: 018623-014600US
; CURRENT APPLICATION NUMBER: US/09/458,298
; CURRENT FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2436
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1658
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-458-298-1658

Query Match          47.3%; Score 26; DB 18; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 WEYF 4
            |:||
            5 WQYF 8

RESULT 14
US-09-458-298A-78
; Sequence 78, Application US/09458298A
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130000
; CURRENT APPLICATION NUMBER: US/09/458,298A
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; NUMBER OF SEQ ID NOS: 2436
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 454
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-458-298A-78

Query Match          47.3%; Score 26; DB 18; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 WEYF 4
            |:||
            5 WQYF 8

RESULT 15
US-09-458-298A-454
; Sequence 454, Application US/09458298A
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130000
; CURRENT APPLICATION NUMBER: US/09/458,298A
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2438
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 454
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-458-298A-454

Query Match          47.3%; Score 26; DB 18; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 WEYF 4
            |:||
            5 WQYF 4

Search completed: September 16, 2005, 12:10:49
Job time : 445 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:57:54 ; Search time 152 Seconds
(without alignments)
26.640 Million cell updates/sec

Title: US-10-795-795-6

Perfect score: 55

Sequence: 1 WEYFIAAEV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 219186

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	10	US-09-911-1298-6
2	55	100.0	10	16	US-10-795-795-6
3	33	60.0	10	10	US-09-911-1298-5
4	33	60.0	10	16	US-10-795-795-5
5	29	52.7	9	9	US-09-748-451-19
6	27	49.1	10	17	US-10-937-912-105
7	26	47.3	6	15	US-10-353-419A-5
8	26	47.3	8	15	US-10-149-135-78
9	26	47.3	8	15	US-10-149-135-454
10	26	47.3	8	15	US-10-149-135-772
11	26	47.3	8	15	US-10-149-135-1276

12	26	47.3	8	15	US-10-149-135-1279	Sequence 1279, Ap
13	26	47.3	8	15	US-10-149-135-1654	Sequence 1654, Ap
14	26	47.3	8	15	US-10-149-135-1658	Sequence 1658, Ap
15	26	47.3	9	14	US-10-062-109A-101	Sequence 101, App
16	26	47.3	9	14	US-10-062-109A-372	Sequence 372, App
17	26	47.3	9	14	US-10-062-109A-657	Sequence 657, App
18	26	47.3	9	14	US-10-005-480A-101	Sequence 101, App
19	26	47.3	9	14	US-10-005-480A-372	Sequence 372, App
20	26	47.3	9	14	US-10-005-480A-657	Sequence 657, App
21	26	47.3	9	15	US-10-447-161-26	Sequence 26, Appl
22	26	47.3	9	15	US-10-149-135-74	Sequence 74, Appl
23	26	47.3	9	15	US-10-149-135-79	Sequence 79, Appl
24	26	47.3	9	15	US-10-149-135-732	Sequence 732, App
25	26	47.3	9	15	US-10-149-135-759	Sequence 759, App
26	26	47.3	9	15	US-10-149-135-773	Sequence 773, App
27	26	47.3	9	15	US-10-149-135-1266	Sequence 1266, Ap
28	26	47.3	9	15	US-10-149-135-1277	Sequence 1277, Ap
29	26	47.3	9	15	US-10-149-135-1280	Sequence 1280, Ap
30	26	47.3	9	15	US-10-149-135-1642	Sequence 1642, Ap
31	26	47.3	9	15	US-10-149-135-1659	Sequence 1659, Ap
32	26	47.3	9	15	US-10-149-135-1904	Sequence 1904, Ap
33	26	47.3	9	15	US-10-149-135-2144	Sequence 2144, Ap
34	26	47.3	10	14	US-10-062-109A-151	Sequence 151, App
35	26	47.3	10	14	US-10-062-109A-207	Sequence 207, App
36	26	47.3	10	14	US-10-062-109A-421	Sequence 421, App
37	26	47.3	10	14	US-10-062-109A-545	Sequence 545, App
38	26	47.3	10	14	US-10-062-109A-637	Sequence 637, App
39	26	47.3	10	14	US-10-005-480A-151	Sequence 151, App
40	26	47.3	10	14	US-10-005-480A-207	Sequence 207, App
41	26	47.3	10	14	US-10-005-480A-421	Sequence 421, App
42	26	47.3	10	14	US-10-005-480A-545	Sequence 545, App
43	26	47.3	10	14	US-10-005-480A-637	Sequence 637, App
44	26	47.3	10	15	US-10-149-135-50	Sequence 50, Appl
45	26	47.3	10	15	US-10-149-135-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-09-911-1298-6
; Sequence 6, Application US/099111298
; Publication No. US20030040600A1
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalfatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,1298
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-1298-6

Query Match 100.0%; Score 55; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYFIAAEV 10
| | | | | | | | | |
DB 1 WEYFIAAEV 10

RESULT 2
US-10-795-795-6
; Sequence 6, Application US/10795795
; Publication No. US20040186271A1
; GENERAL INFORMATION:

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; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; CURRENT FILING DATE: 2004-03-08
; PRIOR FILING DATE: US/09/911,129B
; PRIOR APPLICATION NUMBER: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-795-795-6

Query Match      100.0%; Score 55; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYFIAAEV 10
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Db      1 WEYFIAAEV 10

RESULT 3
US-09-911-129B-5
; Sequence 5, Application US/0911129B
; Publication No. US20030040600A1
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,129B
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-129B-5

Query Match      60.0%; Score 33; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYFI 5
      |||||
Db      6 WEYFI 10

RESULT 4
US-10-795-795-5
; Sequence 5, Application US/10795795
; Publication No. US20040186271A1
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; CURRENT FILING DATE: 2004-03-08
; PRIOR FILING DATE: US/09/911,129B
; PRIOR APPLICATION NUMBER: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-795-795-5

Query Match      60.0%; Score 33; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYFI 5
      |||||
Db      6 WEYFI 10

Query Match      60.0%; Score 33; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYFI 5
      |||||
Db      6 WEYFI 10

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-795-795-5

Query Match      60.0%; Score 33; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYFI 5
      |||||
Db      6 WEYFI 10

RESULT 5
US-09-748-451-19
; Sequence 19, Application US/09748451
; Patent No. US20010011078A1
; GENERAL INFORMATION:
; APPLICANT: WANG, XIAODONG
; APPLICANT: LIU, XUESONG
; TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS
; FILE REFERENCE: UTSD:546USD1
; CURRENT APPLICATION NUMBER: US/09/748,451
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/061,702
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-748-451-19

Query Match      52.7%; Score 29; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
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Db      4 WEYF 7

RESULT 6
US-10-937-912-105
; Sequence 105, Application US/10937912
; Publication No. US20050090448A1
; GENERAL INFORMATION:
; APPLICANT: Baxter International Inc.
; APPLICANT: Johnson, Richard J
; APPLICANT: Maves, Shelley A
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT COMPLEMENT ACTIVATION
; FILE REFERENCE: TR-6067 (BXTR 4017.1)
; CURRENT APPLICATION NUMBER: US/10/937,912
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/501,710
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: complement inhibitor
US-10-937-912-105

Query Match      49.1%; Score 27; DB 17; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYFI 5
      |||:
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Db          6 WEPFL 10

RESULT 7
US-10-353-419A-5
; Sequence 5, Application US/10353419A
; Publication No. US20030224987A1
; GENERAL INFORMATION:
; APPLICANT: Ryu, Sung-ho
; APPLICANT: Suh, Pann-Ghill
; APPLICANT: Bae, Yoe-Sik
; APPLICANT: Song, Ji-Young
; TITLE OF INVENTION: Immune Modulating Peptides
; FILE REFERENCE: AP34977 072944.0167
; CURRENT APPLICATION NUMBER: US/10/353,419A
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/352,930
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Immune-modulating peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 6
; OTHER INFORMATION: D-Met
US-10-353-419A-5

Query Match          47.3%; Score 26; DB 15; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 WEYFI 5
      |||
Db      1 WEYMV 5

RESULT 8
US-10-149-135-78
; Sequence 78, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 454
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-78

Query Match          47.3%; Score 26; DB 15; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
      |||
Db      1 WQYF 4

RESULT 9
US-10-149-135-454
; Sequence 454, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 454
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-454

Query Match          47.3%; Score 26; DB 15; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
      |||
Db      1 WQYF 4

RESULT 10
US-10-149-135-772
; Sequence 772, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
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; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidnev, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 772
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-772

Query Match          47.3%; Score 26; DB 15; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEYF 4
Db      5 WQYF 8
      |:|||

RESULT 11
US-10-149-135-1276
; Sequence 1276, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidnev, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1276
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1276

Query Match          47.3%; Score 26; DB 15; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEYF 4
Db      5 WQYF 8
      |:|||

RESULT 12
US-10-149-135-1279
; Sequence 1279, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidnev, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1279
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1279

Query Match          47.3%; Score 26; DB 15; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEYF 4
Db      1 WQYF 4
      |:|||

RESULT 13
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US-10-149-135-1654
; Sequence 1654, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1654
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1654

Query Match 47.3%; Score 26; DB 15; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
DB 4 WQYF 7

RESULT 14
US-10-149-135-1658
; Sequence 1658, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713

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; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1658
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1658

Query Match 47.3%; Score 26; DB 15; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
DB 5 WQYF 8

RESULT 15
US-10-062-109A-101
; Sequence 101, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubbert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F108 Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-101

Query Match 47.3%; Score 26; DB 14; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
DB 3 WQYF 6

Search completed: September 16, 2005, 12:16:26
Job time : 153 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:46:58 ; Search time 38.6667 Seconds
(without alignments)
19.306 Million cell updates/sec

Title: US-10-795-795-6
Perfect score: 55
Sequence: 1 WEYFIAAEV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 115489

Minimum DB seq length: 3
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA:*
- 1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*
 - 2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
 - 3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*
 - 4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
 - 5: /cgn2_6/prodata/1/iaa/6C COMB.pcp.*
 - 6: /cgn2_6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	4	US-09-911-129B-6
2	33	60.0	10	4	US-09-911-129B-5
3	29	52.7	9	3	US-09-061-702-19
4	29	52.7	9	4	US-09-748-451-19
5	26	47.3	8	3	US-08-649-100-23
6	26	47.3	8	3	US-08-649-100-39
7	26	47.3	9	3	US-08-159-339A-1218
8	26	47.3	10	3	US-08-159-339A-1219
9	25	45.5	6	1	US-08-121-202-8
10	24	43.6	4	3	US-09-315-304B-1565
11	24	43.6	4	4	US-09-350-325-25
12	24	43.6	4	4	US-09-350-641C-1565
13	24	43.6	5	1	US-08-068-947-2
14	24	43.6	5	3	US-09-315-304B-1566
15	24	43.6	5	4	US-09-350-325-26
16	24	43.6	5	4	US-09-350-641C-1566
17	24	43.6	6	1	US-08-433-318A-14
18	24	43.6	6	1	US-08-433-318A-15
19	24	43.6	6	1	US-08-433-318A-16
20	24	43.6	6	1	US-08-433-318A-17
21	24	43.6	6	2	US-08-922-048-14
22	24	43.6	6	2	US-08-922-048-15
23	24	43.6	6	2	US-08-922-048-16
24	24	43.6	6	2	US-08-922-048-17
25	24	43.6	6	3	US-09-315-304B-1567
26	24	43.6	6	3	US-09-315-304B-1568
27	24	43.6	6	3	US-09-315-304B-1569

28	24	43.6	6	4	US-09-111-681C-30	Sequence 30, Appl
29	24	43.6	6	4	US-09-111-681C-31	Sequence 31, Appl
30	24	43.6	6	4	US-09-111-681C-32	Sequence 32, Appl
31	24	43.6	6	4	US-09-111-681C-33	Sequence 33, Appl
32	24	43.6	6	4	US-09-350-325-27	Sequence 27, Appl
33	24	43.6	6	4	US-09-350-325-43	Sequence 43, Appl
34	24	43.6	6	4	US-09-350-325-46	Sequence 46, Appl
35	24	43.6	6	4	US-09-350-641C-1567	Sequence 1567, Ap
36	24	43.6	6	4	US-09-350-641C-1583	Sequence 1583, Ap
37	24	43.6	6	4	US-09-350-641C-1586	Sequence 1586, Ap
38	24	43.6	6	5	PCT-US96-06270-14	Sequence 14, Appl
39	24	43.6	6	5	PCT-US96-06270-15	Sequence 15, Appl
40	24	43.6	6	5	PCT-US96-06270-16	Sequence 16, Appl
41	24	43.6	6	5	PCT-US96-06270-17	Sequence 17, Appl
42	24	43.6	7	2	US-08-188-583-45	Sequence 45, Appl
43	24	43.6	8	2	US-08-188-583-50	Sequence 50, Appl
44	24	43.6	8	3	US-09-082-279B-1433	Sequence 1433, Ap
45	24	43.6	8	3	US-09-082-279B-1474	Sequence 1474, Ap

ALIGNMENTS

RESULT 1
US-09-911-129B-6
; Sequence 6, Application US/09911129B
; Patent No. 6703364
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,129B
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-129B-6

Query Match 100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYFIAAEV 10
| | | | | | | | | |
Db 1 WEYFIAAEV 10

RESULT 2
US-09-911-129B-5
; Sequence 5, Application US/09911129B
; Patent No. 6703364
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,129B
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-129B-5

Query Match 60.0%; Score 33; DB 4; Length 10;

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Best Local Similarity 100.0%; Pred. No. 4.1; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 WEYFI 5
    |||||
Db 6 WEYFI 10

RESULT 3
US-09-061-702-19
; Sequence 19, Application US/09061702
; Patent No. 6165737
; GENERAL INFORMATION:
; APPLICANT: Wang, Xiaodong
; APPLICANT: Liu, Xuesong
; TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN
; TITLE OF INVENTION: APOPTOSIS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,702
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: UTSD:546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512)418-3000
; TELEFAX: (512)474-7577
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-061-702-19

Query Match 52.7%; Score 29; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
    |||||
Db 4 WEYF 7

RESULT 4
US-09-748-451-19
; Sequence 19, Application US/09748451
; Patent No. 6790648
; GENERAL INFORMATION:
; APPLICANT: WANG, XIAODONG
; APPLICANT: LIU, XUESONG
; TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS
; FILE REFERENCE: UTSD:546USD1
; CURRENT APPLICATION NUMBER: US/09/748,451
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/061,702
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1

Query Match 47.3%; Score 26; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
    |||||
Db 3 WEYF 6

RESULT 6
US-08-649-100-39
; Sequence 39, Application US/08649100
; Patent No. 6114507
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; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-748-451-19

Query Match 52.7%; Score 29; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
    |||||
Db 4 WEYF 7

RESULT 5
US-08-649-100-23
; Sequence 23, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUE, TOMOKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: CO. MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-649-100-23

Query Match 47.3%; Score 26; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
    |||||
Db 3 WEYF 6

RESULT 6
US-08-649-100-39
; Sequence 39, Application US/08649100
; Patent No. 6114507
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; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUE, TOMOKAZU
; APPLICANT: NAGATA, SHIGEKAZU
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-PAS LIGAND ANTIBODY AND ASSAY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/649,100
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-649-100-39

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Query Match 47.3%; Score 26; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 WEYF 4
   |::|
Db 3 WDYF 6

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RESULT 7
US-08-159-339A-1218
; Sequence 1218, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-1218

Query Match 47.3%; Score 26; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
   |::|
Db 2 WDYF 5

RESULT 8
US-08-159-339A-1219
; Sequence 1219, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993

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US-09-350-641C-1565
; Sequence 1565, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1565
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641C-1565

Query Match 43.6%; Score 24; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
DB 1 WYWF 4

RESULT 13
US-08-068-947-2
; Sequence 2, Application US/08068947
; Patent No. 5470753
; GENERAL INFORMATION:
; APPLICANT: Sepetov, Nikolai
; APPLICANT: Lessakova, Olga
; APPLICANT: Krchnak, Viktor
; APPLICANT: Lebl, Michal
; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
; TITLE OF INVENTION: SPECTROMETRY
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,947
; FILING DATE: 19930528
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock Esq., S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-040-999
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE

US-09-350-641C-1566
; Sequence 1566, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1867
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1566
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1566

Query Match 43.6%; Score 24; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
DB 2 WYWF 5

RESULT 14
US-09-315-304B-1566
; Sequence 1566, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1867
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1566
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1566

Query Match 43.6%; Score 24; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
DB 2 WYWF 5

RESULT 15
US-09-350-325-26
; Sequence 26, Application US/09350325
; Patent No. 6541020
; GENERAL INFORMATION:
; APPLICANT: Ding, S.
; APPLICANT: Kang, M.
; APPLICANT: Venetta, T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF
; TITLE OF INVENTION: THERAPEUTIC REAGENTS
; FILE REFERENCE: 7872-062
; CURRENT APPLICATION NUMBER: US/09/350,325
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: enhancer peptide
US-09-350-325-26

Query Match      43.6%; Score 24; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
        |||
Db      2 WEMF 5

Search completed: September 16, 2005, 11:59:36
Job time : 38.6667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:45:28 ; Search time 74 Seconds
(without alignments)

34.600 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LDNFS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 2547

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	73.1	10	2	P96305
2	18	69.2	7	1	FARB CALVO
3	18	69.2	10	1	FARB CALVO
4	17	65.4	8	2	Q6Z269
5	17	65.4	10	1	TKNB RANRI
6	16	61.5	8	1	AKHG GRYBI
7	16	61.5	8	1	AKH ROMMI
8	16	61.5	8	1	HTFI PERAM
9	16	61.5	8	1	HTF TENMO
10	16	61.5	8	1	HTF ZOPRU
11	16	61.5	8	1	RPCH PANBO
12	16	61.5	8	2	Q9RSR0
13	16	61.5	9	2	Q7KYP6
14	16	61.5	9	2	Q93LE4
15	16	61.5	9	2	Q9RSR1
16	16	61.5	10	1	HTF BLAGE
17	16	61.5	10	1	HTF GROPO
18	16	61.5	10	1	HTF LEUMA
19	16	61.5	10	1	HTF NAUCI
20	16	61.5	10	2	Q7MA65
21	16	61.5	10	2	Q9TRA9
22	16	61.5	10	2	Q96423
23	16	61.5	10	2	Q8VHM9
24	15	57.7	8	2	Q9N6M5
25	15	57.7	9	2	Q14715
26	15	57.7	9	2	Q71UH0
27	15	57.7	10	2	Q7M3D3
28	15	57.7	10	2	Q9LSW6
29	14	53.8	8	2	Q7X139
30	14	53.8	9	2	Q96T78
31	14	53.8	9	2	Q9XJN0

32 14 53.8 10 1 URA7 HUMAN
33 13 50.0 8 1 AKH GEOST
34 13 50.0 8 1 AKH LIBAU
35 13 50.0 8 1 AKH MELML
36 13 50.0 8 1 AKH PACMA
37 13 50.0 8 1 ALJ6 CYDPO
38 13 50.0 8 2 P87225
39 13 50.0 8 2 Q7M4H6
40 13 50.0 8 2 Q7M4H7
41 13 50.0 8 2 Q94VF3
42 13 50.0 8 2 Q7LZ21
43 13 50.0 9 1 FAR8 MACRS
44 13 50.0 9 2 Q6LE76
45 13 50.0 9 2 Q7M2M7

P34990 homo sapien
P84241 geotrupes s
P25418 libellula a
P84240 melolontha
P84242 pachnoda ma
P82157 cydia pomon
P87225 saccharomyc
Q7mdh6 ischnura se
Q7mdh7 pseudagrion
Q94vf3 varanus kei
Q7l221 gallus gall
P83281 macrobrachi
Q6le76 homo sapien
Q7m2m7 bos taurus

ALIGNMENTS

RESULT 1
P96305 PRELIMINARY; PRT; 10 AA.
AC P96305;
DT 01-MAY-1997 (TREMREL. 03, Created)
DT 01-MAY-1997 (TREMREL. 03, Last sequence update)
DT 01-MAR-2002 (TREMREL. 20, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Alteromonas haloplanktis (Pseudoalteromonas haloplanktis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Pseudoalteromonadaceae; Pseudoalteromonas.
OX NCBI_TaxID=228;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14393;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
DR EMBL; U68076; AAB48021.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1053 MW; 857BD235AB544AAA CRC64;

Query Match 73.1%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
Db 4 DNYS 7

RESULT 2
FARB CALVO STANDARD; PRT; 7 AA.
ID FARB CALVO
AC P41866;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CallifMRamide 11.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.

RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Dave H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifMRamides) from the blowfly Calliphora vomitoria.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; B44787; B44787.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 7 7 Phenylalanine amide.
SQ SEQUENCE 7 AA; 926 MW; 69D40699C44AB700 CRC64;

Query Match 69.2%; Score 18; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4
DB 2 DNF 4

RESULT 3
FARC_CALVO STANDARD; PRT; 10 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CalliFMRFamide 12.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly Calliphora
RT vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; C44787; C44787.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 10 10 Phenylalanine amide.
SQ SEQUENCE 10 AA; 1156 MW; 22810399C44AB6D8 CRC64;

Query Match 69.2%; Score 18; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4
DB 5 DNF 7

RESULT 4
Q6Z269 PRELIMINARY; PRT; 8 AA.
AC Q6Z269;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE RNA polymerase II (Fragment).
GN Name=rp2;
OS Silene ajanensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=265238;
RN [1]

```

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RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Popp M., Oxelman B.;
RT "Evolution of a RNA polymerase gene family in Silene (Caryophyllaceae)
RT incomplete concerted evolution and topological congruence among
RT paralogues.";
RL Syst. Biol. 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Popp M.;
RT "Disentangling the reticulate history of polyploids in Silene
RT (Caryophyllaceae).";
RL Thesis (2004), Department of Evolutionary Biology, Systematic Botany,
RL Uppsala universitet, Uppsala, Sweden.
DR EMBL; AJ634075; CAG24094.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 859 MW; 892DD325B0544AB2 CRC64;

Query Match 65.4%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDNFS 5
DB 1 VDNIS 5

RESULT 5
TKNB_RANRI STANDARD; PRT; 10 AA.
AC P29135;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neurokinin A.
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=93075037; PubMed=1332683;
RA Wang Y., Badgery-Parker T., Lovas S., Chartrel N., Vaudry H.,
RA Burcher E., Conlon J.M.;
RT "Primary structure and receptor-binding properties of a neurokinin A-
RT related peptide from frog gut.";
RL Biochem. J. 287:827-832(1992).
CC -|- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S27178; S27178.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD_RES 10 10 Methionine amide.
SQ SEQUENCE 10 AA; 1160 MW; 526B407059D5BAA7 CRC64;

Query Match 65.4%; Score 17; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNF 4
DB 3 LDSP 6

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RESULT 6
AKHG GRVBI STANDARD; PRT; 8 AA.
ID AC P67785; P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipokinetic hormone G (AKH-G).
OS Gryllus bimaculatus (two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=8810653; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
of a peptide with adipokinetic activity from the corpora cardiaca of
the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914 (1987).
CC -1- FUNCTION: This hormone, released from cells in the corpora
cardiaca after the beginning of flight, causes release of
diglycerides from the fat body and then stimulates the flight
muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A28004; A28004.
DR InterPro; IPR02047; AKH.
DR PROSITE; PS00256; AKH; 1.
RW Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT MOD RES 8 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 61.5%; Score 16; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
DB 3 NFS 5

RESULT 7
AKHG ROWMI STANDARD; PRT; 8 AA.
ID AC P67786; P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipokinetic hormone (AKH) (RO II).
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948; DOI=10.1016/0196-9781(88)90107-6;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688 (1988).
CC -1- FUNCTION: This hormone, released from cells in the corpora
cardiaca after the beginning of flight, causes release of
diglycerides from the fat body and then stimulates the flight
muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A28004; A28004.
DR InterPro; IPR02047; AKH.
DR PROSITE; PS00256; AKH; 1.
RW Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT MOD RES 8 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 61.5%; Score 16; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
DB 3 NFS 5

RESULT 8
HTF1 PERAM STANDARD; PRT; 8 AA.
ID AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypertrahalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
DE (PeA-CAH-I) (LeD-CC-I) (Hypertrahalosaemic neuropeptide I).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358 (1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
cardioacceleratory and hyperglycemic activity from the corpora
cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579 (1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128; DOI=10.1016/0196-9781(89)90023-5;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiacum from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289 (1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrahalosaemic neuropeptides isolated from
the corpora cardiaca of the cockroaches Leucophaea maderae,
Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
CC -1- FUNCTION: Hypertrahalosaemic factors are neuropeptides that
elevate the level of trehalose in the hemolymph (trehalose is the

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DR InterPro; IPR02047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT MOD RES 8 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 61.5%; Score 16; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
DB 3 NFS 5

RESULT 8
HTF1 PERAM STANDARD; PRT; 8 AA.
ID AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypertrahalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
DE (PeA-CAH-I) (LeD-CC-I) (Hypertrahalosaemic neuropeptide I).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358 (1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
cardioacceleratory and hyperglycemic activity from the corpora
cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579 (1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128; DOI=10.1016/0196-9781(89)90023-5;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiacum from the potato
beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289 (1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrahalosaemic neuropeptides isolated from
the corpora cardiaca of the cockroaches Leucophaea maderae,
Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
CC -1- FUNCTION: Hypertrahalosaemic factors are neuropeptides that
elevate the level of trehalose in the hemolymph (trehalose is the

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CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A05169; A05169.
DR PIR; A44960; A44960.
DR PIR; A49823; A49823.
DR PIR; S08995; S08995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Neuropeptide;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 Pyroglutamate carboxylic acid.
FT MOD_RES 8 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 61.5%; Score 16; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
DB |||
3 NFS 5

RESULT 9
HTF TENMO STANDARD; PRT; 8 AA.
AC P67789; P25419;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypertrehalosemic factor (HOTH) (Hypertrehalosemic neuropeptide).
OS Tenebrio molitor (Yellow mealworm).
CC -1- FUNCTION: Hypertrehalosemic factors are neuropeptides that
elevate the level of trehalose in the hemolymph of insects).
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A43976; A43976.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Neuropeptide;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 Pyroglutamate carboxylic acid.
FT MOD_RES 8 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 61.5%; Score 16; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
DB |||
3 NFS 5

RESULT 10
HTF ZOPRU STANDARD; PRT; 8 AA.
AC P67790; P25419;
DT 01-MAY-1992 (Rel. 22, Created)

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DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypertrehalosemic factor (HOTH) (Hypertrehalosemic neuropeptide).
OS Zophobas rugipes.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Zophobas.
OX NCBI_TaxID=7075;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90341081; PubMed=2381871; DOI=10.1016/0196-9781(90)90042-4;
RA Gaede G., Rosinski G.;
RT "The primary structure of the hypertrehalosemic neuropeptide from
Tenebrionid beetles: a novel member of the AKH/RPCH family.";
RL Peptides 11:455-459(1990).
CC -1- FUNCTION: Hypertrehalosemic factors are neuropeptides that
elevate the level of trehalose in the hemolymph of insects).
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; B43976; B43976.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Neuropeptide;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 Pyroglutamate carboxylic acid.
FT MOD_RES 8 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 61.5%; Score 16; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
DB |||
3 NFS 5

RESULT 11
RPCH PANBO STANDARD; PRT; 8 AA.
AC P08939;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Red pigment concentrating hormone (RPCH).
OS Pandanus borealis (Northern red shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
OC Pandallidae; Pandalus.
OX NCBI_TaxID=6703;
RN [1]
RP SEQUENCE.
RX MEDLINE=75054965; PubMed=4433569;
RA Fernlund P.;
RT "Structure of the red-pigment-concentrating hormone of the shrimp,
Pandanus borealis.";
RL Biochim. Biophys. Acta 371:304-311(1974).
CC -1- FUNCTION: This hormone adapts the animal to light backgrounds by
stimulating concentration of the pigment of its red body-
chromatophores.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A61348; A61348.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Hormone; Pigment;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 Pyroglutamate carboxylic acid.
FT MOD_RES 8 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;

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Query Match 61.5%; Score 16; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
Db 3 NFS 5

RESULT 12
Q9RSR0 PRELIMINARY; PRT; 8 AA.
AC Q9RSR0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 11,500 DA product of ORFA (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
RN [1]
RP SEQUENCE.
RX MEDLINE=92085268; PubMed=1660923;
RA Polard P., Prere M.F., Chandler M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an AUU codon
in gene expression of bacterial insertion sequence IS911.";
RL J. Mol. Biol. 222:465-477(1991).
FT NON TER 8
SQ SEQUENCE 8 AA; 935 MW; F4C5B9C45AE33336 CRC64;

Query Match 61.5%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
Db 5 NFS 7

RESULT 13
Q7KYP6 PRELIMINARY; PRT; 9 AA.
AC Q7KYP6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Mi.V glycoprotein (exon P3B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Miltenberger class V;
RX MEDLINE=30005483; PubMed=2792104;
RA Vignal A., Rahuel C., El-Malliki B., London J., Le Vankim C.,
RA Blanchard C.D.;
RT "Molecular Analysis of glycoprotein A and B gene structure and
expression . . . .";
RL Eur. J. Biochem. 184:337-344(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Miltenberger class V;
RX MEDLINE=30005483; PubMed=2792104;
RA Vignal A., Rahuel C., El-Malliki B., London J., Le Vankim C.,
RA Blanchard C.D.;
RT "Molecular Analysis of glycoprotein A and B gene structure and
expression . . . .";
RL Eur. J. Biochem. 184:0-0(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Miltenberger class V;
RA Cartton J.P.;

Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
DR EMBL; X15824; CAA33822.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1073 MW; 50D145B7244AB403 CRC64;

Query Match 61.5%; Score 16; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNFS 5
Db 4 DNLS 7

RESULT 14
Q93LE4 PRELIMINARY; PRT; 9 AA.
ID Q93LE4;
AC Q93LE4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Proteolysis tag (Fragment).
OS Helicobacillus mobilis.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;
OC Helicobacillus.
OX NCBI_TaxID=28064;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063247; PubMed=10592213; DOI=10.1093/nar/28.1.168;
RA Williams K.P.;
RT "The tmRNA website.";
RL Nucleic Acids Res. 28:168-168(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Williams K.P.;
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY040838; AAK83526.1; -.
FT NON TER 1
SQ SEQUENCE 9 AA; 937 MW; 7CD8D72DCB544AAB CRC64;

Query Match 61.5%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
Db 3 DNYS 6

RESULT 15
Q9RSR1 PRELIMINARY; PRT; 9 AA.
ID Q9RSR1;
AC Q9RSR1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Putative transposase (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
RN [1]
RP SEQUENCE.
RX MEDLINE=92085268; PubMed=1660923;
RA Polard P., Prere M.F., Chandler M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an AUU codon
in gene expression of bacterial insertion sequence IS911.";
RL J. Mol. Biol. 222:465-477(1991).
DR PIR; S19523; S19523.
FT NON TER 9
SQ SEQUENCE 9 AA; 1063 MW; 5EB4C5B9C45AE333 CRC64;

Query Match 61.5%; Score 16; DB 2; Length 9;
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Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
|||
Db 5 NFS 7

Search completed: September 16, 2005, 11:57:41
Job time : 75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:54:04 ; Search time 32.6667 Seconds
(without alignments)
25.020 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LDNFS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 760079 seqs, 163465437 residues

Total number of hits satisfying chosen parameters: 87311

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:

- 1: /cgn2_6/ptodata/2/paa/PCT NEW COMB.pap.*
- 2: /cgn2_6/ptodata/2/paa/US06 NEW COMB.pap.*
- 3: /cgn2_6/ptodata/2/paa/US07 NEW COMB.pap.*
- 4: /cgn2_6/ptodata/2/paa/US08 NEW COMB.pap.*
- 5: /cgn2_6/ptodata/2/paa/US09 NEW COMB.pap.*
- 6: /cgn2_6/ptodata/2/paa/US10 NEW COMB.pap.*
- 7: /cgn2_6/ptodata/2/paa/US11 NEW COMB.pap.*
- 8: /cgn2_6/ptodata/2/paa/US60 NEW COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	76.9	8	5	US-09-908-943B-11
2	20	76.9	8	5	US-09-908-943B-65
3	20	76.9	8	5	US-09-908-943B-66
4	20	76.9	8	5	US-09-908-943B-67
5	20	76.9	8	5	US-09-908-943B-72
6	20	76.9	10	1	PCT-US05-16441-17
7	19	73.1	5	7	US-11-004-399-2954
8	19	73.1	6	7	US-11-078-203-5
9	19	73.1	7	7	US-11-028-230-2
10	19	73.1	7	7	US-11-028-230-4
11	19	73.1	9	6	US-10-817-970-1350
12	19	73.1	9	6	US-10-817-970-3476
13	19	73.1	9	6	US-10-817-970-3573
14	19	73.1	10	1	PCT-US04-39285-218
15	19	73.1	10	6	US-10-817-970-3762
16	19	73.1	10	6	US-10-817-970-14569
17	18	69.2	6	7	US-10-538-310-3
18	18	69.2	6	7	US-11-032-773-42
19	18	69.2	8	5	US-09-908-943B-68
20	18	69.2	8	5	US-11-111-072-15
21	18	69.2	8	8	US-60-701-050-2524
22	18	69.2	9	5	US-09-583-200E-48
23	18	69.2	9	5	US-09-189-702B-184
24	18	69.2	9	6	US-10-817-970-184
25	18	69.2	9	6	US-10-817-970-3225

26	18	69.2	9	6	US-10-817-970-3449	Sequence 3449, Ap
27	18	69.2	9	6	US-10-817-970-3480	Sequence 3480, Ap
28	18	69.2	9	6	US-10-817-970-3501	Sequence 3501, Ap
29	18	69.2	9	6	US-10-817-970-3517	Sequence 3517, Ap
30	18	69.2	9	6	US-10-817-970-3574	Sequence 3574, Ap
31	18	69.2	9	6	US-10-817-970-3636	Sequence 3636, Ap
32	18	69.2	9	6	US-10-817-970-14629	Sequence 14629, A
33	18	69.2	9	6	US-10-953-901-651	Sequence 651, App
34	18	69.2	9	6	US-10-538-066-753	Sequence 753, App
35	18	69.2	9	7	US-11-041-893-27	Sequence 27, Appl
36	18	69.2	9	7	US-11-051-411-1202	Sequence 1202, Ap
37	18	69.2	9	7	US-11-051-411-1346	Sequence 1346, Ap
38	18	69.2	9	7	US-11-045-024-14223	Sequence 14223, A
39	18	69.2	9	7	US-11-045-024-14505	Sequence 14505, A
40	18	69.2	9	7	US-11-208-541-4	Sequence 4, Appl
41	18	69.2	10	1	PCT-US05-04900-2	Sequence 2, Appl
42	18	69.2	10	7	US-11-057-708-20	Sequence 20, Appl
43	18	69.2	10	7	US-11-019-894A-30	Sequence 30, Appl
44	17	65.4	7	6	US-10-395-607A-194	Sequence 194, App
45	17	65.4	7	7	US-11-202-009-3469	Sequence 3469, Ap

ALIGNMENTS

RESULT 1

US-09-908-943B-11
; Sequence 11, Application US/09908943B
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrikson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US
; CURRENT APPLICATION NUMBER: US/09/908,943B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-09-908-943B-11

Query Match 76.9%; Score 20; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNF 4

Db :||| 7

RESULT 2

US-09-908-943B-65
; Sequence 65, Application US/09908943B
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrikson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US

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; CURRENT APPLICATION NUMBER: US/09/908,943B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa= E, G, I, D, T, cysteic acid or S
US-09-908-943B-65

Query Match          76.9%; Score 20; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDNF 4
Db      :|||
        4 MDNF 7

RESULT 3
US-09-908-943B-66
; Sequence 66, Application US/09908943B
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Robert L.
; APPLICANT: Heinrikson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US
; CURRENT APPLICATION NUMBER: US/09/908,943B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa= A, V, I, S, H, Y, T or F
US-09-908-943B-66

Query Match          76.9%; Score 20; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDNF 4
Db      :|||
        4 MDNF 7

RESULT 4
US-09-908-943B-67
; Sequence 67, Application US/09908943B
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Robert L.
; APPLICANT: Heinrikson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US
; CURRENT APPLICATION NUMBER: US/09/908,943B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa= F, W, G, A, H, P, G, N or S
US-09-908-943B-72

Query Match          76.9%; Score 20; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDNF 4
Db      :|||
        4 MDNF 7

RESULT 5
US-09-908-943B-72
; Sequence 72, Application US/09908943B
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrikson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US
; CURRENT APPLICATION NUMBER: US/09/908,943B
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa= F, W, G, A, H, P, G, N or S
US-09-908-943B-72

Query Match          76.9%; Score 20; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDNF 4
Db      :|||
        4 MDNF 7
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RESULT 6
PCT-US05-16441-17
; Sequence 17, Application PC/TUS0516441
; GENERAL INFORMATION:
; APPLICANT: Abgenomics Corporation
; TITLE OF INVENTION: T-CELL DEATH-INDUCING EPITOPES
; FILE REFERENCE: 113062-009W01
; CURRENT APPLICATION NUMBER: PCT/US05/16441
; PRIOR FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
PCT-US05-16441-17

Query Match 76.9%; Score 20; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNP 4
DB 3 MDNF 6

RESULT 7
US-11-004-399-2954
; Sequence 2954, Application US/11004399
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SA
; FILE REFERENCE: 2587/73166/RDX
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR FILING DATE: 2004-12-03
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2954
; LENGTH: 5
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399-2954

Query Match 73.1%; Score 19; DB 7; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
DB 2 DNFA 5

RESULT 8
US-11-078-203-5
; Sequence 5, Application US/11078203
; GENERAL INFORMATION:
; APPLICANT: Pak, Brian
; APPLICANT: Fu, Siyu
; APPLICANT: Lomas, Lee
; APPLICANT: Tornatore, Pete
```

```
; APPLICANT: Viner, Rosa
; APPLICANT: Weinberger, Scot R.
; APPLICANT: Yip, Tai-tung
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: SARS Virus Polypeptides
; FILE REFERENCE: 016866-010671US
; CURRENT APPLICATION NUMBER: US/11/078,203
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/461,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/462,597
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/462,928
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/462,964
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/463,177
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/463,874
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/470,688
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 10/822,152
; PRIOR FILING DATE: 2004-04-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: severe acute
; OTHER INFORMATION: respiratory syndrome (SARS)-related polypeptide
; OTHER INFORMATION: trypsin digest Peptide 5
US-11-078-203-5

Query Match 73.1%; Score 19; DB 7; Length 6;
Best Local Similarity 60.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5
DB 1 MDDFS 5

RESULT 9
US-11-028-230-2
; Sequence 2, Application US/11028230
; GENERAL INFORMATION:
; APPLICANT: SHIMADZU CORPORATION
; TITLE OF INVENTION: Method for Selective Measurement of Specific Substances from a Mi:
; TITLE OF INVENTION: MALDI Mass Spectrometry
; FILE REFERENCE: G16-32-US
; CURRENT APPLICATION NUMBER: US/11/028,230
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: JP2004-153484
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: JP2004-368508
; PRIOR FILING DATE: 2004-12-20
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Gallus gallus
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: 6
; OTHER INFORMATION: NITRATION
US-11-028-230-2

Query Match 73.1%; Score 19; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDNF 4
|||:
Db 3 LDNY 6

RESULT 10

US-11-028-230-4
; Sequence 4, Application US/11028230
; GENERAL INFORMATION:
; APPLICANT: SHIMADZU CORPORATION
; TITLE OF INVENTION: Method for Selective Measurement of Specific Substances from a Mixture
; FILE REFERENCE: MALDI Mass Spectrometry
; CURRENT APPLICATION NUMBER: US/11/028,230
; PRIOR FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: JP2004-153484
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: JP2004-368508
; PRIOR FILING DATE: 2004-12-20
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-028-230-4

Query Match 73.1%; Score 19; DB 7; Length 7;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNF 4
|||:
Db 3 LDNY 6

RESULT 11

US-10-817-970-1350
; Sequence 1350, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.050000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1350
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-1350

Query Match 73.1%; Score 19; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
|||:
Db 5 DNFA 8

RESULT 12

US-10-817-970-3476
; Sequence 3476, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.050000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3476
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-3476

Query Match 73.1%; Score 19; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
|||:
Db 5 DNFA 8

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; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Biomolecule
; OTHER INFORMATION: partition motif
PCT-US04-39285-218

Query Match      73.1%; Score 19; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDNF 4
Db      1 VDNF 4

RESULT 13
US-10-817-970-3573
; Sequence 3573, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.0500000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3573
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-3573

Query Match      73.1%; Score 19; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNFS 5
Db      5 DNFA 8

RESULT 14
PCT-US04-39285-218
; Sequence 218, Application PC/TUS0439285
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: BIOMOLECULE PARTITION MOTIFS AND USES THEREOF
; FILE REFERENCE: (71699)62360 PCT
; CURRENT APPLICATION NUMBER: PCT/US04/39285
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/524,380
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 332
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 218
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Biomolecule
; OTHER INFORMATION: partition motif
PCT-US04-39285-218

Query Match      73.1%; Score 19; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDNF 4
Db      1 VDNF 4

RESULT 15
US-10-817-970-3762
; Sequence 3762, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.0500000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3762
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-3762

Query Match      73.1%; Score 19; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNFS 5
Db      7 DNFA 10

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Job time : 33.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:49:59 ; Search time 222 Seconds
(without alignments)
26.306 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LDNFS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 755392

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgm2_6/ptodata/1/paa/US080_COMB.pep.*
- 5: /cgm2_6/ptodata/1/paa/US081_COMB.pep.*
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- 37: /cgm2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	26	100.0	5	33	US-10-795-795-12	Sequence 12, Appl
2	26	100.0	10	33	US-10-795-795-11	Sequence 11, Appl
3	22	84.6	8	27	US-10-111-983-2406	Sequence 2406, Ap
4	22	84.6	8	27	US-10-111-983-16504	Sequence 16504, A
5	22	84.6	8	27	US-10-111-983-28478	Sequence 28478, A
6	22	84.6	9	8	US-08-457-540A-33	Sequence 33, Appl
7	22	84.6	9	19	US-09-519-658A-43	Sequence 43, Appl
8	22	84.6	10	19	US-09-573-822C-408	Sequence 408, App
9	22	84.6	10	19	US-09-573-822D-408	Sequence 408, App
10	21	80.8	8	7	US-08-334-029A-6	Sequence 6, Appl
11	21	80.8	8	33	US-10-768-798-6	Sequence 33494, A
12	20	76.9	5	27	US-10-111-983-33494	Sequence 33494, A
13	20	76.9	6	27	US-10-111-983-33453	Sequence 33453, A
14	20	76.9	7	18	US-09-403-092-2	Sequence 2, Appl
15	20	76.9	7	21	US-09-749-234-2	Sequence 2, Appl
16	20	76.9	7	21	US-09-749-234A-2	Sequence 2, Appl
17	20	76.9	8	1	PCT-US02-02303-97	Sequence 97, Appl
18	20	76.9	8	24	US-09-908-943A-11	Sequence 11, Appl
19	20	76.9	8	24	US-09-908-943A-65	Sequence 65, Appl
20	20	76.9	8	24	US-09-908-943A-66	Sequence 66, Appl
21	20	76.9	8	24	US-09-908-943A-67	Sequence 67, Appl
22	20	76.9	8	24	US-09-908-943A-72	Sequence 72, Appl
23	20	76.9	8	34	US-10-801-486-11	Sequence 11, Appl
24	20	76.9	8	34	US-10-801-486-65	Sequence 65, Appl
25	20	76.9	8	34	US-10-801-486-66	Sequence 66, Appl
26	20	76.9	8	34	US-10-801-486-67	Sequence 67, Appl
27	20	76.9	8	34	US-10-801-486-72	Sequence 72, Appl
28	20	76.9	8	34	US-10-801-487-11	Sequence 11, Appl
29	20	76.9	8	34	US-10-801-487-65	Sequence 65, Appl
30	20	76.9	8	34	US-10-801-487-66	Sequence 66, Appl
31	20	76.9	8	34	US-10-801-487-67	Sequence 67, Appl
32	20	76.9	8	34	US-10-801-487-72	Sequence 72, Appl
33	20	76.9	8	34	US-10-801-493-11	Sequence 11, Appl
34	20	76.9	8	34	US-10-801-493-65	Sequence 65, Appl
35	20	76.9	8	34	US-10-801-493-66	Sequence 66, Appl
36	20	76.9	8	34	US-10-801-493-67	Sequence 67, Appl
37	20	76.9	8	34	US-10-801-493-72	Sequence 72, Appl
38	20	76.9	8	34	US-10-801-509-11	Sequence 11, Appl
39	20	76.9	8	34	US-10-801-509-65	Sequence 65, Appl
40	20	76.9	8	34	US-10-801-509-66	Sequence 66, Appl
41	20	76.9	8	34	US-10-801-509-67	Sequence 67, Appl
42	20	76.9	8	34	US-10-801-509-72	Sequence 72, Appl
43	20	76.9	8	34	US-10-801-938-11	Sequence 11, Appl
44	20	76.9	8	34	US-10-801-938-65	Sequence 65, Appl
45	20	76.9	8	34	US-10-801-938-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-10-795-795-12
; Sequence 12, Application US/10795795
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-795-795-12

Query Match 100.0%; Score 26; DB 33; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNFS 5
 Db 1 LDNFS 5

RESULT 2

US-10-795-795-11
 ; Sequence 11, Application US/10795795
 ; GENERAL INFORMATION:
 ; APPLICANT: Cleveland State University
 ; APPLICANT: Kalafatis, Michael
 ; APPLICANT: Mann, Kenneth G.
 ; TITLE OF INVENTION: Thrombin Generation Inhibitor
 ; FILE REFERENCE: 27433/04004
 ; CURRENT APPLICATION NUMBER: US/10/795,795
 ; CURRENT FILING DATE: 2004-03-08
 ; PRIOR APPLICATION NUMBER: US/09/911,129B
 ; PRIOR FILING DATE: 2002-03-19
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-795-795-11

Query Match 100.0%; Score 26; DB 33; Length 10;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNFS 5
 Db 6 LDNFS 10

RESULT 3

US-10-111-983-2406
 ; Sequence 2406, Application US/10111983
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: GALEOTTI Cesira
 ; APPLICANT: GRANDI Guido
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MORA Mariarosa
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: RAPPUOLI Rino
 ; APPLICANT: RATTI Giulio
 ; APPLICANT: SCARLATO Vincenzo
 ; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
 ; FILE REFERENCE: 2300-1654 (PP01654.003)
 ; CURRENT APPLICATION NUMBER: US/10/111,983
 ; CURRENT FILING DATE: 2003-06-27
 ; PRIOR APPLICATION NUMBER: US-60/162616
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 37764
 ; SOFTWARE: SeqWin99, version 1.02
 ; SEQ ID NO 2406
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Neisseria
 US-10-111-983-2406

Query Match 84.6%; Score 22; DB 27; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
 Db 2 LDNF 5

RESULT 4

US-10-111-983-16504
 ; Sequence 16504, Application US/10111983
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: GALEOTTI Cesira
 ; APPLICANT: GRANDI Guido
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MORA Mariarosa
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: RAPPUOLI Rino
 ; APPLICANT: RATTI Giulio
 ; APPLICANT: SCARLATO Vincenzo
 ; APPLICANT: SCARSELLI Maria
 ; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
 ; FILE REFERENCE: 2300-1654 (PP01654.003)
 ; CURRENT APPLICATION NUMBER: US/10/111,983
 ; CURRENT FILING DATE: 2003-06-27
 ; PRIOR APPLICATION NUMBER: US-60/162616
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 37764
 ; SOFTWARE: SeqWin99, version 1.02
 ; SEQ ID NO 16504
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Neisseria
 US-10-111-983-16504

Query Match 84.6%; Score 22; DB 27; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
 Db 2 LDNF 5

RESULT 5

US-10-111-983-28478
 ; Sequence 28478, Application US/10111983
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: GALEOTTI Cesira
 ; APPLICANT: GRANDI Guido
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MORA Mariarosa
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: RAPPUOLI Rino
 ; APPLICANT: RATTI Giulio
 ; APPLICANT: SCARLATO Vincenzo
 ; APPLICANT: SCARSELLI Maria
 ; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
 ; FILE REFERENCE: 2300-1654 (PP01654.003)
 ; CURRENT APPLICATION NUMBER: US/10/111,983
 ; CURRENT FILING DATE: 2003-06-27
 ; PRIOR APPLICATION NUMBER: US-60/162616
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 37764
 ; SOFTWARE: SeqWin99, version 1.02
 ; SEQ ID NO 28478
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Neisseria
 US-10-111-983-28478

Query Match 84.6%; Score 22; DB 27; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
Db 2 LDNF 5

RESULT 6
US-08-457-540A-33
; Sequence 33, Application US/08457540A
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, SONIA L.
; APPLICANT: PANACCIO, MICHAEL
; APPLICANT: WILSON, LACHLAN R.
; APPLICANT: WIJFELS, GENE L.
; APPLICANT: SPIETHILL, TERENCE W.
; APPLICANT: CAMPBELL, NOEL J.
; APPLICANT: THOMPSON, CATRIONA M.
; APPLICANT: SEXTON, JENNIFER L.
; APPLICANT: MILNER, ANDREW R.
; APPLICANT: MITCHELL, GRAHAM F.
; TITLE OF INVENTION: VACCINE FOR THE PREVENTATIVE TREATMENT
; OF INFECTION OF LIVER FLUKE IN RUMINANTS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,540A
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,061
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/730,895
; FILING DATE: 31-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU90/00027
; FILING DATE: 31-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU 872481
; FILING DATE: 31-JAN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 218067/1747488/JMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-457-540A-33

Query Match 84.6%; Score 22; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDNF 4

Db 6 LDNF 9

RESULT 7
US-09-519-658A-43
; Sequence 43, Application US/09519658A
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH et al.
; TITLE OF INVENTION: Tumor-associated antigen
; FILE REFERENCE: seq12202
; CURRENT APPLICATION NUMBER: US/09/519,658A
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-519-658A-43

Query Match 84.6%; Score 22; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
Db 2 LDNF 5

RESULT 8
US-09-573-822C-408
; Sequence 408, Application US/09573822C
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 408
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG189 at 100-109 and may interact with Sequen
; OTHER INFORMATION: in this patent.
US-09-573-822C-408

Query Match 84.6%; Score 22; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
Db 1 DNFS 4

RESULT 9
US-09-573-822D-408
; Sequence 408, Application US/09573822D
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822D
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 892
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 408
; LENGTH: 10
; TYPE: PRT

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; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG189 at 100-109 and may interact with Sequen
; OTHER INFORMATION: in this patent.
US-09-573-822D-408

Query Match      84.6%; Score 22; DB 19; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DNFS 5
Db      1 DNFS 4

RESULT 10
US-08-334-029A-6
; Sequence 6, Application US/08334029A
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Haleboua, Simon
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Drug Screening,
; TITLE OF INVENTION: and Methods of Making and Using Thereof
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,029A
; FILING DATE: 02-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: 1459.0240000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-334-029A-6

Query Match      80.8%; Score 21; DB 7; Length 8;
Best Local Similarity 60.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDNFS 5
Db      4 IDNFS 8

RESULT 11
US-10-768-798-6
; Sequence 6, Application US/10768798
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Haleboua, Simon
; TITLE OF INVENTION: Peripheral Nervous System Specific
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; Sodium Channels, DNA Encoding Thereof, Crystallization,
; X-ray Diffraction, Computer Molecular Modeling, Rational
; Drug Design, Drug Screening, and Methods of Making and Using
;
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/768,798
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/457,571
; FILING DATE: 09-DEC-1999
; APPLICATION NUMBER: 08/836,325
; FILING DATE: 02-MAY-1997
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0917.0240003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-768-798-6

Query Match      80.8%; Score 21; DB 33; Length 8;
Best Local Similarity 60.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LDNFS 5
Db      4 IDNFS 8

RESULT 12
US-10-111-983-33494
; Sequence 33494, Application US/10111983
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: GALEOTTI Cesira
; APPLICANT: GRANDI Guido
; APPLICANT: MASIGNANI Vega
; APPLICANT: MORA Mariarosa
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: RAPPUOLI Rino
; APPLICANT: RATTI Giulio
; APPLICANT: SCARLATO Vincenzo
; APPLICANT: SCARSELLI Maria
; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
; FILE REFERENCE: 2300-1654 (PP01654.003)
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; CURRENT APPLICATION NUMBER: US/10/111.983
 ; CURRENT FILING DATE: 2003-06-27
 ; PRIOR APPLICATION NUMBER: US-60/162616
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 37764
 ; SOFTWARE: SeqWin99, version 1.02
 ; SEQ ID NO 33494
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Neisseria
 US-10-111-983-33494

Query Match 76.9%; Score 20; DB 27; Length 5;
 Best Local Similarity 75.0%; Pred. No. 6.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNF 4
 :|||
 Db 1 IDNF 4

RESULT 13

US-10-111-983-33453
 ; Sequence 33453, Application US/10111983
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: GALEOTTI Cesira
 ; APPLICANT: GRANDI Guido
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MORA Mariarosa
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: RAPPUOLI Rino
 ; APPLICANT: RATTI Giulio
 ; APPLICANT: SCARLATO Vincenzo
 ; APPLICANT: SCARSELLI Maria
 ; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
 ; FILE REFERENCE: 2300-1654 (PP01654.003)
 ; CURRENT APPLICATION NUMBER: US/10/111.983
 ; CURRENT FILING DATE: 2003-06-27
 ; PRIOR APPLICATION NUMBER: US-60/162616
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 37764
 ; SOFTWARE: SeqWin99, version 1.02
 ; SEQ ID NO 33453
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Neisseria
 US-10-111-983-33453

Query Match 76.9%; Score 20; DB 27; Length 6;
 Best Local Similarity 80.0%; Pred. No. 6.4e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDNFS 5
 :|||
 Db 2 LDRFS 6

RESULT 14

US-09-403-092-2
 ; Sequence 2, Application US/09403092
 ; GENERAL INFORMATION:
 ; APPLICANT: HOFMANN, Joachim
 ; APPLICANT: SCHMID, Karlheirich
 ; APPLICANT: PAULI, Annette
 ; TITLE OF INVENTION: DICTYOCALUS VIVIPARUS ANTIGEN FOR THE
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNGWORM INFESTATION AND FOR VACCINATION
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY & LARDNER
 ; STREET: 3000 K Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.

; COUNTRY: U.S.A.
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/403,092
 ; FILING DATE: 15-OCT-1999
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/EP98/02090
 ; FILING DATE: 09-APR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 197 15 586.3
 ; FILING DATE: 15-APR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granados, Patricia D.
 ; REGISTRATION NUMBER: 33,683
 ; REFERENCE/DOCKET NUMBER: 038311/0103
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-403-092-2

Query Match 76.9%; Score 20; DB 18; Length 7;
 Best Local Similarity 75.0%; Pred. No. 6.4e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNF 4
 :|||
 Db 2 MDNF 5

RESULT 15

US-09-749-234-2
 ; Sequence 2, Application US/09749234
 ; GENERAL INFORMATION:
 ; APPLICANT: HOFMANN, Joachim
 ; SCHMID, Karlheirich
 ; PAULI, Annette

; TITLE OF INVENTION: DICTYOCALUS VIVIPARUS ANTIGEN FOR THE
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNGWORM INFESTATION AND FOR VACCINATION
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY & LARDNER
 ; STREET: 3000 K Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20007-5109

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/749,234
 ; FILING DATE: 27-Dec-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/403,092
 ; FILING DATE: 1999-10-15
 ; APPLICATION NUMBER: DE 197 15 586.3
 ; FILING DATE: 15-APR-1997

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: Granados, Patricia D.
/ REGISTRATION NUMBER: 33,683
/ REFERENCE/DOCKET NUMBER: 038311/0103
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 672-5300
/ TELEFAX: (202) 672-5399
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-749-234-2

Query Match      76.9%; Score 20; DB 21; Length 7;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDNF 4
        :|||
Db       2 MDNF 5

Search completed: September 16, 2005, 12:10:49
Job time : 222 secs
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OM protein - protein search, using sw model

Run on: September 16, 2005, 11:57:54 ; Search time 76 Seconds
(without alignments)

26.640 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LDNFS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 219186

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	5	10	US-09-911-1298-12
2	26	100.0	5	16	US-10-795-795-12
3	26	100.0	10	10	US-09-911-1298-11
4	26	100.0	10	16	US-10-795-795-11
5	22	84.6	10	10	US-09-573-822C-408
6	21	80.8	8	10	US-09-457-571-6
7	21	80.8	8	16	US-10-768-798-6
8	20	76.9	7	9	US-09-749-234A-2
9	20	76.9	8	10	US-09-908-943A-11
10	20	76.9	8	10	US-09-908-943A-65
11	20	76.9	8	10	US-09-908-943A-66

12	20	76.9	8	10	US-09-908-943A-67	Sequence 67, Appl
13	20	76.9	8	10	US-09-908-943A-72	Sequence 72, Appl
14	20	76.9	8	16	US-10-801-487-11	Sequence 11, Appl
15	20	76.9	8	16	US-10-801-487-65	Sequence 65, Appl
16	20	76.9	8	16	US-10-801-487-66	Sequence 66, Appl
17	20	76.9	8	16	US-10-801-487-72	Sequence 72, Appl
18	20	76.9	8	16	US-10-801-487-72	Sequence 72, Appl
19	20	76.9	8	16	US-10-801-938-11	Sequence 11, Appl
20	20	76.9	8	16	US-10-801-938-65	Sequence 65, Appl
21	20	76.9	8	16	US-10-801-938-66	Sequence 66, Appl
22	20	76.9	8	16	US-10-801-938-67	Sequence 67, Appl
23	20	76.9	8	16	US-10-801-938-72	Sequence 72, Appl
24	20	76.9	8	16	US-10-801-509-11	Sequence 11, Appl
25	20	76.9	8	16	US-10-801-509-65	Sequence 65, Appl
26	20	76.9	8	16	US-10-801-509-66	Sequence 66, Appl
27	20	76.9	8	16	US-10-801-509-67	Sequence 67, Appl
28	20	76.9	8	16	US-10-801-509-72	Sequence 72, Appl
29	20	76.9	8	16	US-10-801-486-11	Sequence 11, Appl
30	20	76.9	8	16	US-10-801-486-65	Sequence 65, Appl
31	20	76.9	8	16	US-10-801-486-66	Sequence 66, Appl
32	20	76.9	8	16	US-10-801-486-67	Sequence 67, Appl
33	20	76.9	8	16	US-10-801-486-72	Sequence 72, Appl
34	20	76.9	8	17	US-10-801-493-11	Sequence 11, Appl
35	20	76.9	8	17	US-10-801-493-65	Sequence 65, Appl
36	20	76.9	8	17	US-10-801-493-66	Sequence 66, Appl
37	20	76.9	8	17	US-10-801-493-67	Sequence 67, Appl
38	20	76.9	8	17	US-10-801-493-72	Sequence 72, Appl
39	20	76.9	9	14	US-10-119-536A-111	Sequence 111, Appl
40	20	76.9	10	15	US-10-601-837-9	Sequence 9, Appl
41	19	73.1	5	15	US-10-436-549-13	Sequence 13, Appl
42	19	73.1	5	16	US-10-712-425-13	Sequence 13, Appl
43	19	73.1	5	17	US-10-808-187-2261	Sequence 2261, Appl
44	19	73.1	5	17	US-10-773-032-13	Sequence 13, Appl
45	19	73.1	5	18	US-10-807-807-2261	Sequence 2261, Appl

ALIGNMENTS

RESULT 1
US-09-911-1298-12
; Sequence 12, Application US/099111298
; Publication No. US20030040600A1
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,1298
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-1298-12

Query Match 100.0%; Score 26; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNFS 5
| | | | |
Db 1 LDNFS 5

RESULT 2
US-10-795-795-12
; Sequence 12, Application US/10795795
; Publication No. US20040186271A1
; GENERAL INFORMATION:

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; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-795-795-12
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Query Match 100.0%; Score 26; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDNFS 5
    |||||
Db 1 LDNFS 5
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RESULT 3
US-09-911-129B-11
; Sequence 11, Application US/09911129B
; Publication No. US20030040600A1
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,129B
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-129B-11
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Query Match 100.0%; Score 26; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDNFS 5
    |||||
Db 6 LDNFS 10
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RESULT 4
US-10-795-795-11
; Sequence 11, Application US/10795795
; Publication No. US20040186271A1
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 10
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-795-795-11
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Query Match 100.0%; Score 26; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDNFS 5
    |||||
Db 6 LDNFS 10
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RESULT 5
US-09-573-822C-408
; Sequence 408, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 408
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG189 at 100-109 and may interact with Sequen
; OTHER INFORMATION: in this patent.
US-09-573-822C-408
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Query Match 84.6%; Score 22; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 DNFS 5
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Db 1 DNFS 4
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RESULT 6
US-09-457-571-6
; Sequence 6, Application US/09457571
; Publication No. US20030092645A1
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/457,571
; FILING DATE: 09-DEC-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA: PCT/US95/14251
APPLICATION NUMBER: 02-NOV-1995
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-457-571-6

Query Match 80.8%; Score 21; DB 10; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5
DB 4 IDNFN 8

RESULT 7
US-10-768-798-6
Sequence 6, Application US/10768798
Publication No. US20040229792A1
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
Sodium Channels, DNA Encoding therefor, Crystallization,
X-ray Diffraction, Computer Molecular Modeling, Rational
Drug Design, Drug Screening, and Methods of Making and Using
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/768,798
FILING DATE: 29-Jan-2004
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995

APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-768-798-6

Query Match 80.8%; Score 21; DB 16; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5
DB 4 IDNFN 8

RESULT 8
US-09-749-234A-2
Sequence 2, Application US/09749234A
Patent No. US20020068817A1
GENERAL INFORMATION:
APPLICANT: HOFMANN, Joachim
SCHMID, Karlheirich
PAULI, Annette
TITLE OF INVENTION: DICTYOCALUS VIVIPARUS ANTIGEN FOR THE
DIAGNOSIS OF LUNGWORM INFESTATION AND FOR VACCINATION
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,234A
FILING DATE: 27-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/403,092
FILING DATE: 199-10-15
APPLICATION NUMBER: DE 197 15 586.3
FILING DATE: 15-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 038311/0103
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-749-234A-2

Query Match          76.9%; Score 20; DB 9; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNF 4
   :|||
Db  2 MDNF 5

RESULT 9
US-09-908-943A-11
; Sequence 11, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrichson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-09-908-943A-11

Query Match          76.9%; Score 20; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNF 4
   :|||
Db  4 MDNF 7

RESULT 10
US-09-908-943A-65
; Sequence 65, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrichson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-09-908-943A-65

Query Match          76.9%; Score 20; DB 9; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNF 4
   :|||
Db  4 MDNF 7

RESULT 11
US-09-908-943A-66
; Sequence 66, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrichson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-09-908-943A-66

Query Match          76.9%; Score 20; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNF 4
   :|||
Db  4 MDNF 7

RESULT 12
US-09-908-943A-67
; Sequence 67, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrichson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-09-908-943A-67
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; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa= N, L, K, S, G, T, D, A, Q or E
US-09-908-943A-67

Query Match          76.9%; Score 20; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
Db :|||
4 MDNF 7

RESULT 13
US-09-908-943A-72
; Sequence 72, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tonasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrichson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa= F, W, G, A, H, P, G, N or S
US-09-908-943A-72

Query Match          76.9%; Score 20; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
Db :|||
4 MDNF 7

RESULT 14
US-10-801-487-11
; Sequence 11, Application US/10801487
; Publication No. US20040241792A1
; GENERAL INFORMATION:
; APPLICANT: Yan et al.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281F
; CURRENT APPLICATION NUMBER: US/10/801,487
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; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 09/908,943
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-10-801-487-11

Query Match          76.9%; Score 20; DB 16; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
Db :|||
4 MDNF 7

RESULT 15
US-10-801-487-65
; Sequence 65, Application US/10801487
; Publication No. US20040241792A1
; GENERAL INFORMATION:
; APPLICANT: Yan et al.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281F
; CURRENT APPLICATION NUMBER: US/10/801,487
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 09/908,943
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa= E, G, I, D, T, cysteic acid or S
US-10-801-487-65

Query Match          76.9%; Score 20; DB 16; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
Db :|||
4 MDNF 7

Search completed: September 16, 2005, 12:16:27
Job time : 77 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2005, 11:46:58 ; Search time 19.3333 Seconds
(without alignments)
19.306 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LDNFS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 115489

Minimum DB seq length: 3

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	5	4	US-09-911-129B-12
2	26	100.0	10	4	US-09-911-129B-11
3	21	80.8	8	3	US-08-836-325-6
4	21	80.8	8	4	US-09-457-571-6
5	19	73.1	7	4	US-09-822-270-5
6	18	69.2	6	1	US-07-932-200-3
7	18	69.2	6	2	US-08-387-749-3
8	18	69.2	6	2	US-08-845-742-4
9	18	69.2	6	5	PCT-US91-08231-3
10	18	69.2	7	2	US-08-687-702-22
11	18	69.2	7	4	US-09-721-870-122
12	18	69.2	7	4	US-09-721-870-123
13	18	69.2	7	4	US-09-693-746-27
14	18	69.2	7	4	US-09-693-746-143
15	18	69.2	7	4	US-09-693-746-146
16	18	69.2	8	1	US-08-462-894-23
17	18	69.2	8	1	US-08-206-185-23
18	18	69.2	8	2	US-08-669-284B-33
19	18	69.2	8	4	US-09-388-413B-3
20	18	69.2	8	4	US-10-233-745-3
21	18	69.2	9	1	US-08-447-500-26
22	18	69.2	9	1	US-08-454-097-26
23	18	69.2	9	1	US-08-453-866-26
24	18	69.2	9	2	US-08-359-705B-36
25	18	69.2	9	2	US-08-340-283-203
26	18	69.2	9	2	US-08-286-846A-36
27	18	69.2	9	2	US-08-457-880A-36

28 18 69.2 9 2 US-08-318-856A-1 Sequence 1, Appli
29 18 69.2 9 3 US-08-444-622A-36 Sequence 36, Appl
30 18 69.2 9 3 US-08-942-562-36 Sequence 36, Appl
31 18 69.2 9 3 US-08-159-339A-128 Sequence 128, App
32 18 69.2 9 3 US-08-185-359-26 Sequence 26, Appl
33 18 69.2 9 3 US-09-156-923-36 Sequence 36, Appl
34 18 69.2 9 4 US-08-197-484-21 Sequence 21, Appl
35 18 69.2 9 4 US-09-543-608A-48 Sequence 48, Appl
36 18 69.2 9 4 US-09-454-204A-6 Sequence 6, Appli
37 18 69.2 9 4 US-09-239-043D-2492 Sequence 2492, Ap
38 18 69.2 9 4 US-09-763-397A-9 Sequence 9, Appli
39 18 69.2 9 4 US-09-693-746-32 Sequence 32, Appl
40 18 69.2 9 5 PCT-US95-02121-21 Sequence 21, Appl
41 18 69.2 10 1 US-08-229-515A-1 Sequence 1, Appli
42 18 69.2 10 1 US-08-645-865-1 Sequence 1, Appli
43 18 69.2 10 5 PCT-US93-08067-4 Sequence 4, Appli
44 17 65.4 5 4 US-09-788-006-163 Sequence 163, App
45 17 65.4 6 1 US-08-136-743B-62 Sequence 62, Appl

ALIGNMENTS

RESULT 1

US-09-911-129B-12

; Sequence 12, Application US/09911129B

; Patent No. 6703364

; GENERAL INFORMATION:

; APPLICANT: Cleveland State University

; APPLICANT: Kalafatis, Michael

; APPLICANT: Mann, Kenneth G.

; TITLE OF INVENTION: Thrombin Generation Inhibitor

; FILE REFERENCE: 27433/04004

; CURRENT APPLICATION NUMBER: US/09/911,129B

; CURRENT FILING DATE: 2002-03-19

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-911-129B-12

Query Match 100.0%; Score 26; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.1e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5

DB 1 LDNFS 5

RESULT 2

US-09-911-129B-11

; Sequence 11, Application US/09911129B

; Patent No. 6703364

; GENERAL INFORMATION:

; APPLICANT: Cleveland State University

; APPLICANT: Kalafatis, Michael

; APPLICANT: Mann, Kenneth G.

; TITLE OF INVENTION: Thrombin Generation Inhibitor

; FILE REFERENCE: 27433/04004

; CURRENT APPLICATION NUMBER: US/09/911,129B

; CURRENT FILING DATE: 2002-03-19

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-911-129B-11

Query Match 100.0%; Score 26; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 6.2; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 LDNFS 5
Db 6 LDNFS 10

RESULT 3
US-08-836-325-6
; Sequence 6, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Haleboua, Simon
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/836,325
; FILING DATE: 2-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,325
; FILING DATE: 02-NOV-1995
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0917.0240002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-325-6

Query Match 80.8%; Score 21; DB 3; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5
Db 4 IDNFN 8

RESULT 4

US-09-457-571-6
; Sequence 6, Application US/09457571
; Patent No. 6703486
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Haleboua, Simon
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/457,571
; FILING DATE: 09-DEC-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,325
; FILING DATE: 02-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0917.0240003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-457-571-6

Query Match 80.8%; Score 21; DB 4; Length 8;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5
Db 4 IDNFN 8

RESULT 5

US-09-822-270-5
; Sequence 5, Application US/09822270
; Patent No. 6559126
; GENERAL INFORMATION:
; APPLICANT: TOURNAIRE, ROSELYNE
; APPLICANT: DEMANGEL, CAROLINE
; APPLICANT: DERBIN, CLAUDE

APPLICANT: PERRET, GERARD
APPLICANT: MAZIE, JEAN-CLAUDE
APPLICANT: PLOUET, JEAN
APPLICANT: VASSAY, ROGER
TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIA
TITLE OF INVENTION: ANGIOGENESIS, POLYNUCLEOTIDES ENCODING SAID PEPTIDES AND METHODS
FILE REFERENCE: 205060U0
CURRENT APPLICATION NUMBER: US/09/822,270
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 60/193,396
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 7
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-822-270-5

Query Match 73.1%; Score 19; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNP 4
DB 2 LDNY 5

RESULT 6
US-07-932-200-3
Sequence 3, Application US/07932200
Patent No. 5366862
GENERAL INFORMATION:
APPLICANT: VENTON, DUANE L.
APPLICANT: HOPFINGER, ANTON J.
APPLICANT: LE BRETTON, GUY
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
TITLE OF INVENTION: USEFUL PEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/932,200
FILING DATE: 21-AUG-1992
CLASSIFICATION: 435
NAME: COOPER, IVER P.
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENTON=1B
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-932-200-3

Query Match 69.2%; Score 18; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4
DB 4 DNF 6

RESULT 7
US-08-387-749-3
Sequence 3, Application US/08387749
Patent No. 5814460
GENERAL INFORMATION:
APPLICANT: VENTON, DUANE L.
APPLICANT: HOPFINGER, ANTON J.
APPLICANT: LE BRETTON, GUY
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
TITLE OF INVENTION: USEFUL PEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,749
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
NAME: COOPER, IVER P.
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENTON=IC
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-387-749-3

Query Match 69.2%; Score 18; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 DNF 4
Db      4 DNF 6

RESULT 8
US-08-845-742-4
; Sequence 4, Application US/08845742C
; Patent No. 5973229
; GENERAL INFORMATION:
; APPLICANT: Walton, Jonathan D
; APPLICANT: Scott-Craig, John S
; TITLE OF INVENTION: Gene Encoding Herbicide Safener Binding Protein
; FILE REFERENCE: 6550-000007
; CURRENT APPLICATION NUMBER: US/08/845,742C
; CURRENT FILING DATE: 1997-04-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Zea mays
US-08-845-742-4

Query Match      69.2%; Score 18; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNF 4
Db      4 DNF 6

PCT-US93-08231-3
; MOLECULE TYPE: peptide
Query Match      69.2%; Score 18; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNF 4
Db      4 DNF 6

RESULT 10
US-08-687-702-32
; Sequence 32, Application US/08687702
; Patent No. 5922856
; GENERAL INFORMATION:
; APPLICANT: Fritz, Christian C.
; APPLICANT: Green, Michael R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN CRITICAL
; TITLE OF INVENTION: FOR HIV REPLICATION
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,702
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,551
; FILING DATE: 27-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04020/103001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-687-702-32

Query Match      69.2%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNF 4
Db      5 DNF 7

RESULT 11
US-09-721-870-122
; Sequence 122, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
```

; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721.870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Drosophila
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-721-870-122

Query Match 69.2%; Score 18; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNF 4
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Db 2 DNF 4

RESULT 12

US-09-721-870-123
; Sequence 123, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721.870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Drosophila
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-721-870-123

Query Match 69.2%; Score 18; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNF 4
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Db 2 DNF 4

RESULT 13

US-09-693-746-27
; Sequence 27, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.1cp

; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-27

Query Match 69.2%; Score 18; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNF 4
|||
Db 2 DNF 4

RESULT 14

US-09-693-746-143
; Sequence 143, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.1cp
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-143

Query Match 69.2%; Score 18; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNF 4
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Db 2 DNF 4

RESULT 15

US-09-693-746-146
; Sequence 146, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.1cp
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676

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; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-146

Query Match      69.2%; Score 18; DB 4; Length 7;
Best Local Similarity 100.0%; Pred.No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNF 4
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Db      2 DNF 4

Search completed: September 16, 2005, 11:59:37
Job time : 20.3333 secs
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